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=> d his ful

     FILE 'HCAPLUS' ENTERED AT 16:07:00 ON 07 MAY 2004
L1            50 SEA ABB=ON  ((2 OR TWO?)(W)?HYBRID?(W)?SELECTION? OR ?INTERACT?
                 (W)?TRAP?(W)?ASSAY?)
L2            16 SEA ABB=ON  L1 AND ?PROTEIN?(3A)(?SELECT? OR ?FUSION?)
L3             3 SEA ABB=ON  L1 AND ?DIMERIZ?
L4            18 SEA ABB=ON  L2 OR L3
L5             0 SEA ABB=ON  L4 AND (DNA?(W)(?LIBRARY? OR ?BIND))(3A)?TRANSCRIPT
                 ?(W)(?ACTIVAT?(W)?DOMAIN? OR ?FACTOR?)
L6             0 SEA ABB=ON  L4 AND DNA?(W)(?LIBRARY? OR ?BIND)
L7             0 SEA ABB=ON  L1 AND DNA?(W)(?LIBRARY? OR ?BIND)
L8             8 SEA ABB=ON  L1 AND ?TRANSCRIPT?(W)?ACTIVAT?
L9            22 SEA ABB=ON  L4 OR L8
L10           18 SEA ABB=ON  L9 AND ?GENE?
L11            4 SEA ABB=ON  L1 AND ?DIMER?
L12            4 SEA ABB=ON  L11 AND (DNA? OR ?GENE?)
L13           19 SEA ABB=ON  L10 OR L12 -19 cits from CA Plus (see below for 7 more cits)

     FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, JICST-EPLUS, JAPIO' ENTERED AT
     16:15:17 ON 07 MAY 2004
L14           43 SEA ABB=ON  L13
L15           26 DUP REMOV L14 (17 DUPLICATES REMOVED) 26 cits from other databases

     FILE 'HCAPLUS' ENTERED AT 16:29:43 ON 07 MAY 2004
L16           18 SEA ABB=ON  L1 AND ?LIBRARY?
L17           26 SEA ABB=ON  L13 OR L16
L18            7 SEA ABB=ON  L17 NOT L13 -7 cits from CA Plus
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L1          50 SEA FILE=HCAPLUS ABB=ON  ((2 OR TWO?)(W)?HYBRID?(W)?SELECTION?
               OR ?INTERACT?(W)?TRAP?(W)?ASSAY?)
L2          16 SEA FILE=HCAPLUS ABB=ON  L1 AND ?PROTEIN?(3A)(?SELECT? OR
               ?FUSION?)
L3           3 SEA FILE=HCAPLUS ABB=ON  L1 AND ?DIMERIZ?
L4          18 SEA FILE=HCAPLUS ABB=ON  L2 OR L3
L8           8 SEA FILE=HCAPLUS ABB=ON  L1 AND ?TRANSCRIPT?(W)?ACTIVAT?
L9          22 SEA FILE=HCAPLUS ABB=ON  L4 OR L8
L10         18 SEA FILE=HCAPLUS ABB=ON  L9 AND ?GENE?
L11          4 SEA FILE=HCAPLUS ABB=ON  L1 AND ?DIMER?
L12          4 SEA FILE=HCAPLUS ABB=ON  L11 AND (DNA? OR ?GENE?)
L13         19 SEA FILE=HCAPLUS ABB=ON  L10 OR L12

=> d ibib abs l13 1-19

L13  ANSWER 1 OF 19  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2002:933303  HCAPLUS
DOCUMENT NUMBER:          138:233862
TITLE:                    Multimerization of the Protein-tyrosine Phosphatase
                          (PTP)-like Insulin-dependent Diabetes Mellitus
                          Autoantigens IA-2 and IA-2β with Receptor PTPs
                          (RPTPs). Inhibition of RPTPα enzymatic activity
AUTHOR(S):                Gross, Steffen; Blanchetot, Christophe; Schepens, Jan;
                          Albet, Sabrina; Lammers, Reiner; den Hertog, Jeroen;
                          Hendriks, Wiljan
CORPORATE SOURCE:         Nijmegen Center for Molecular Life Sciences,
                          Department of Cell Biology, University of Nijmegen,
                          Nijmegen, 6525 GA, Germany
SOURCE:                   Journal of Biological Chemistry (2002), 277(50),
                          48139-48145
                          CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER:                American Society for Biochemistry and Molecular
                          Biology
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB   Most receptor-type protein tyrosine phosphatases (RPTPs) contain two
     tandem PTP domains.  For some RPTPs the enzymically inactive
     membrane-distal phosphatase domains (D2) were found to bind enzymically
     active membrane proximal PTP (D1) domains, and oligomerization has been
     proposed as a general regulatory mechanism.  The RPTP-like
     proteins IA-2 and IA-2β, major autoantigens in insulin-dependent
     diabetes mellitus, contain just a single enzymically inactive PTP-like
     domain.  Their physiol. role is as yet enigmatic.  To investigate whether
     the catalytically inactive cytoplasmic domains of IA-2 and IA-2β are
     involved in oligomerization, we exploited interaction
     trap assay in yeast and glutathione S-transferase
     pull-down and co-immunopptn. strategies on lysates of transfected COS-1
     cells.  The results show that IA-2 and IA-2β are capable of homo- and
     heterodimerization to which both the juxtamembrane region and the
     phosphatase-like segment can contribute.  Furthermore, they can form
     heterodimers with some other RPTP members, most notably
     RPTPα and RPTPε, and down-regulate RPTPα enzymic
     activity.  Thus, in addition to homo-dimerization, the enzymic
     activity of receptor-type PTPs can be regulated through
     heterodimerization with other RPTPs, including the catalytically
     inactive IA-2 and IA-2β.
REFERENCE COUNT:          56    THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS
                                RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13  ANSWER 2 OF 19  HCAPLUS  COPYRIGHT 2004 ACS on STN
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ACCESSION NUMBER: 2002:658658 HCAPLUS
DOCUMENT NUMBER: 137:197850
TITLE: Methods and compositions for **interaction trap assays**
INVENTOR(S): Joung, J. Keith; Miller, Jeffrey; Pabo, Carl O.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 61 pp., Cont.-in-part of U.S. Ser. No. 858,852.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002119498	A1	20020829	US 2001-990762	20011114
US 2003044787	A1	20030306	US 2001-858852	20010516

PRIORITY APPLN. INFO.: US 2000-204509P P 20000516
US 2001-858852 A2 20010516

AB The invention concerns methods and compns. for **interaction trap assays** for detecting protein-protein, protein-**DNA**, or protein-RNA interactions. The methods and compns. of the invention may also be used to identify agents which may agonize or antagonize a protein-protein, protein-**DNA**, or protein-RNA interaction. In certain embodiments, the interaction trap system of the invention is useful for screening libraries with greater than 107 members. In other embodiments, the interaction trap system of the invention is used in conjunction with flow cytometry. The invention further provides a means for simultaneously screening a target protein or nucleic acid sequence for the ability to interact with two or more test proteins or nucleic acids.

L13 ANSWER 3 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:332437 HCAPLUS
DOCUMENT NUMBER: 136:339470
TITLE: Identification of epitopes of intracellular proteins using intrabodies and yeast **two-hybrid selection**
INVENTOR(S): Cattaneo, Antonino; Visintin, Michela
PATENT ASSIGNEE(S): S.I.S.S.A. Scuola Internazionale Superiore Di Studi Avanzati, Italy
SOURCE: PCT Int. Appl., 17 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002035237	A2	20020502	WO 2001-IT535	20011022
WO 2002035237	A3	20021010		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,

DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2002015194	A5	20020506	AU 2002-15194	20011022
EP 1328814	A2	20030723	EP 2001-983776	20011022
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
JP 2004512529	T2	20040422	JP 2002-538169	20011022
US 2003235850	A1	20031225	US 2003-418388	20030418
PRIORITY APPLN. INFO.:			IT 2000-RM561 A	20001024
			WO 2001-IT535 W	20011022

AB The authors disclose a method for epitope identification, termed in vivo epitope mapping of specific intracellular antibody (IVEM) comprising the **general** steps of: (a) co-transforming of yeast cells by a first vector expressing the desired antibody fused to the transactivation domain of VP16 and a second vector coding for protein or peptide fused to the DNA-binding domain of LexA; (b) growing co-transformed cells in such an environment that only cells wherein the antibody and the cognate antigen recognize and interact each other allows for growth and replication of the yeast cells; (c) selecting the cells and identification of epitope. In one example, the epitope identification methodol. was applied to mutants of tau protein.

L13 ANSWER 4 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	2002:75438 HCAPLUS
DOCUMENT NUMBER:	137:226954
TITLE:	Yeast and bacterial **two-hybrid** **selection** systems for studying **protein** -protein interactions
AUTHOR(S):	Serebriiskii, Ilya; Joung, J. Keith
CORPORATE SOURCE:	Fox Chase Cancer Center, Philadelphia, PA, 10111, USA
SOURCE:	Protein-Protein Interactions (2002), 93-142. Editor(s): Golemis, Erica. Cold Spring Harbor Laboratory Press: Cold Spring Harbor, N. Y. CODEN: 69CFYI; ISBN: 0-87969-628-1
DOCUMENT TYPE:	Conference; General Review
LANGUAGE:	English

AB A review describes the yeast and bacterial two-hybrid systems as powerful methods for analyzing protein-protein interactions. The screening for novel proteins using the interaction trap variant of the yeast two-hybrid system is discussed. The bacterial two-hybrid system is based on the observation that two interacting proteins X and Y can trigger **transcriptional activation** of a weak promoter in Escherichia coli.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 5 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	2001:114541 HCAPLUS
DOCUMENT NUMBER:	135:206080
TITLE:	**Two-hybrid selection** assay to identify **proteins** interacting with polymerase II transcription factors and regulators
AUTHOR(S):	Petrascheck, Michael; Castagna, Francesca; Barberis, Alcide
CORPORATE SOURCE:	Univ. Zurich, Zurich, Switz.
SOURCE:	BioTechniques (2001), 30(2), 296-298,300,302 CODEN: BTNQDO; ISSN: 0736-6205
PUBLISHER:	Eaton Publishing Co.
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB The RNA polymerase III-based two-hybrid system has been developed to detect interactions between proteins such as RNA polymerase II transcription factors and regulators that cannot be studied by the original RNA polymerase II two-hybrid system. This novel method appears to be most useful for a refined anal. of already known protein-protein interactions. However, the application of this system in library screenings has been impaired by the lack of a suitable assay for the selection of the activated pol III reporter **gene** in yeast. Here, we describe a novel selection assay for the pol III-based two-hybrid system that makes it readily usable for screening expression libraries to search for interacting partners. Our system utilizes a temperature-sensitive (ts) U6 snRNA, which is synthesized by RNA polymerase III from a mutated SNR6 **gene** in yeast. In this ts strain, interactions between hybrid proteins activate an artificial pol III reporter construct (UASG-SNR6), which controls expression of wild-type U6 snRNA. This wild-type U6 snRNA can suppress the ts phenotype and allow growth at the nonpermissive temperature of 37°, thus providing a pos. **selection** system for interacting **proteins.**

REFERENCE COUNT: 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 6 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:446390 HCAPLUS

DOCUMENT NUMBER: 133:162482

TITLE: The PKC targeting protein RACK1 interacts with the Epstein-Barr virus activator protein BZLF1

AUTHOR(S): Baumann, Matthias; Gires, Olivier; Kolch, Walter; Mischak, Harald; Zeidler, Reinhard; Pich, Dagmar; Hammerschmidt, Wolfgang

CORPORATE SOURCE: GSF-National Research Center for Environment and Health, Department of Gene Vectors, Institute of Clinical Molecular Biology and Tumor Genetics, Munchen, D-81377, Germany

SOURCE: European Journal of Biochemistry (2000), 267(12), 3891-3901
CODEN: EJBCAI; ISSN: 0014-2956

PUBLISHER: Blackwell Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Phorbol esters reactivate Epstein-Barr virus (EBV) from latently infected cells via **transcriptional activation** of the viral immediate-early **gene** BZLF1. BZLF1 is a member of the extended AP-1 family of transcription factors that binds to specific BZLF1-binding motifs within early EBV promoters and to consensus AP-1 sites. Regulation of BZLF1's activity is achieved at the transcriptional level as well as through post-translational modifications. Recently, the authors reported that the transcriptional activity of BZLF1 is augmented by TPA. The increase of BZLF1's activity depends on a single Ser residue (S186) that is phosphorylated by protein kinase C (PKC) in vitro and in vivo after stimulation with 12-O-tetradecanoylphorbol-13-acetate (TPA). Here, the authors identified RACK1 as a binding partner of BZLF1 in a yeast **interaction trap assay.** RACK stands for receptor of activated C-kinase and is involved in targeting activated PKCs and other signaling proteins. In vivo, RACK1 binds directly to the transactivation domain of BZLF1. Although a functional relationship between BZLF1 and PKC could be mediated by RACKs, RACK1 did not have a detectable effect on the phosphorylation status of BZLF1 in in vitro or in vivo phosphorylation assays. The authors suggest that RACK1 may act as a scaffolding protein on BZLF1 independently of activated PKCs.

REFERENCE COUNT: 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 7 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:446195 HCAPLUS
DOCUMENT NUMBER: 133:218182
TITLE: A bacterial **two-hybrid** **selection** system for studying **protein** -DNA and protein-protein interactions
AUTHOR(S): Joung, J. Keith; Ramm, Elizabeth I.; Pabo, Carl O.
CORPORATE SOURCE: Howard Hughes Medical Institute and Department of Biology, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2000), 97(13), 7382-7387
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have developed a bacterial "two-hybrid" system that readily allows selection from libraries larger than 108 in size. Our bacterial system may be used to study either protein-DNA or protein-protein interactions, and it offers a number of potentially significant advantages over existing yeast-based one-hybrid and two-hybrid methods. We tested our system by selecting zinc finger variants (from a large randomized library) that bind tightly and specifically to desired DNA target sites. Our method allows sequence-specific zinc fingers to be isolated in a single selection step, and thus it should be more rapid than phage display strategies that typically require multiple enrichment/amplification cycles. Given the large library sizes our bacterial-based selection system can handle, this method should provide a powerful tool for identifying and optimizing protein-DNA and protein-protein interactions.
REFERENCE COUNT: 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 8 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:169142 HCAPLUS
DOCUMENT NUMBER: 133:115751
TITLE: Identification of Drosophila Bicoid-interacting proteins using a custom **two-hybrid** **selection**
AUTHOR(S): Zhu, W.; Hanes, S. D.
CORPORATE SOURCE: School of Public Health, Department of Biomedical Sciences, State University of New York at Albany, Albany, NY, USA
SOURCE: Gene (2000), 245(2), 329-339
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Bicoid directs pattern formation in the developing Drosophila embryo, and does so by performing two seemingly unrelated tasks; it activates transcription and represses translation. To understand how Bicoid carries out this dual role, we sought to identify Bicoid-ancillary proteins that might mediate Bicoid's function in transcription or translation. We used a customized version of the two-hybrid method and found two Bicoid-interacting proteins, Bin1 and Bin3, both of which interact with Bicoid in vitro. Bin1 is similar to a human protein (SAP18) involved in transcription regulation, and Bin3, described in this paper, is similar to a family of protein methyltransferases that modify RNA-binding proteins. Given that Bicoid's role as a translation regulator requires RNA binding,

we suggest that the Bicoid-interacting methyltransferase might be important for that role. The custom two-hybrid method we used, in which Bicoid is bound to DNA via its own DNA binding domain, rather than via a **fusion-protein** tether, should be **generally** applicable to other DNA binding proteins.

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 9 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:755042 HCAPLUS
DOCUMENT NUMBER: 132:89069
TITLE: Cloning of a Schizosaccharomyces pombe homologue of elongation factor 1 alpha by **two-hybrid selection** of calmodulin-binding **proteins**
AUTHOR(S): Rasmussen, Colin; Wiebe, Christine
CORPORATE SOURCE: Department of Anatomy and Cell Biology, University of Saskatchewan, Saskatoon, SK S7N 5E5, Can.
SOURCE: Biochemistry and Cell Biology (1999), 77(5), 421-430
CODEN: BCBIEQ; ISSN: 0829-8211
PUBLISHER: National Research Council of Canada
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This study reports the cloning and characterization of a cDNA encoding elongation factor 1-alpha (EF1α) from the yeast Schizosaccharomyces pombe. The cDNA was cloned from an Schizosaccharomyces pombe expression library by a **two-hybrid selection** for clones encoding calmodulin (CaM)-binding proteins. The predicted protein is highly homologous to mammalian EF1α, indicating a strong tendency towards conservation of the primary amino acid sequence. The protein was expressed as a glutathione S-transferase fusion in both bacteria and in Schizosaccharomyces pombe. The bacterial protein was shown by solution assay to compete with CaM kinase II for CaM. The CaM binding domain was localized to the C-terminus of the protein by this method. Expression of full-length EF1α in vivo caused an increase in cell cycle length and a decreased rate of growth as evidenced by a lack of elongated cells in slowly dividing cultures. This effect appears to involve CaM binding because a truncation mutant version of EF1α lacking the CaM binding domain did not cause cell cycle delay.

REFERENCE COUNT: 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 10 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:450862 HCAPLUS
DOCUMENT NUMBER: 131:83957
TITLE: **Interaction trap assay** and its reagents
INVENTOR(S): Dove, Simon; Joung, J. Keith; Hochschild, Ann
PATENT ASSIGNEE(S): President & Fellows of Harvard College, USA
SOURCE: U.S., 28 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5925523	A	19990720	US 1997-920015	19970826
US 6200759	B1	20010313	US 1999-296204	19990421

PRIORITY APPLN. INFO.: US 1996-24484P P 19960823
US 1997-918612 B2 19970822
US 1997-920015 A1 19970826

AB The present invention makes available an interaction trap system which is derived using recombinantly engineered prokaryotic cells. An interaction trap or two-hybrid system designed for use in a prokaryotic, i.e. bacterial, host is described. The system is **generally** similar to those designed for use with yeast but using components derived solely from prokaryotes. In particular a system using **fusion proteins** of the λ cI repressor that bind an OR2 operator in a modified lacP/O promoter-operator region is described. The second component of the binding assay may be a **fusion protein** of the α or ω subunits of the bacterial RNA polymerase. Alternatively, the LexA repressor may be used in combination with the SOS box.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 11 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:220047 HCAPLUS
DOCUMENT NUMBER: 130:234328
TITLE: Improved yeast **interaction trap assay**
INVENTOR(S): Golemis, Erica; Serebriiskii, Ilya; Khazak, Vladimir
PATENT ASSIGNEE(S): Fox Chase Cancer Center, USA
SOURCE: PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9914319	A1	19990325	WO 1998-US19353	19980916
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2304367	AA	19990325	CA 1998-2304367	19980916
AU 9893180	A1	19990405	AU 1998-93180	19980916
US 6326150	B1	20011204	US 2000-508803	20000316

PRIORITY APPLN. INFO.: US 1997-59065P P 19970916
WO 1998-US19353 W 19980916

AB The invention, which is based upon an adaptation of the existing two-hybrid system, provides novel compns. and methods to facilitate the isolation and characterization of novel, protein-protein interactions involved in the regulation of cell growth and metabolism The invention comprises a dual bait yeast **interaction trap assay**, which improves the accuracy of library screens with an immediate selection to eliminate false positives. The dual bait system of the present invention also allows for comparative, simultaneous assessment of interactions between two related members of a protein family or a wild-type vs. mutated form of the same protein.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 12 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:151232 HCAPLUS
DOCUMENT NUMBER: 128:201791
TITLE: An **interaction trap assay**

system using the λ repressor for use in a bacterial host
INVENTOR(S): Dove, Simon; Joung, J. Keith; Hochschild, Ann
PATENT ASSIGNEE(S): President and Fellows of Harvard College, USA; Dove, Simon; Joung, J. Keith; Hochschild, Ann
SOURCE: PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9807845	A1	19980226	WO 1997-US14860	19970822
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9741596	A1	19980306	AU 1997-41596	19970822

PRIORITY APPLN. INFO.: US 1996-24484P P 19960823
WO 1997-US14860 W 19970822

AB An interaction trap or two-hybrid system designed for use in a prokaryotic, i.e. bacterial, host is described. The system is **generally** similar to those designed for use with yeast but using components derived solely from prokaryotes. In particular a system using **fusion proteins** of the λ cI repressor that bind an OR2 operator in a modified lacP/O promoter-operator region is described. The second component of the binding assay may be a **fusion protein** of the α or ω subunits of the bacterial RNA polymerase. Alternatively, the LexA repressor may be used in combination with the SOS box.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 13 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:577429 HCAPLUS
DOCUMENT NUMBER: 127:274307
TITLE: Specific interactions of the autoantigen L7 with multi-zinc finger protein ZNF7 and ribosomal protein S7
AUTHOR(S): Witte, Stephan; Krawinkel, Ulrich
CORPORATE SOURCE: Fak. Biol., Univ. Konstanz, Konstanz, 78434, Germany
SOURCE: Journal of Biological Chemistry (1997), 272(35), 22243-22247
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The eucaryotic protein L7, which assocs. with the large subunit of ribosomes, has been shown to be a major autoantigen in systemic autoimmune arthritis. The N terminus carries a sequence motif that is similar to the leucine zipper domain of eucaryotic transcription factors. This domain promotes the **homodimerization** of protein L7 through α-helical coiled-coil formation and binds to distinct mRNAs, thereby

inhibiting their cell-free translation. Using a yeast **two-hybrid selection**, we have identified from a Jurkat T lymphoma cDNA library ribosomal protein S7 and the multi-zinc finger protein ZNF7 as proteins that interact with protein L7. A fragment of L7 carrying the leucine zipper-like domain is fully sufficient to mediate these interactions. Their potential biol. significance is indicated by low apparent dissociation consts. of S7-L7 (15+10-9 M) and, resp., ZNF7-L7 (2+10-9 M) complexes and coimmunopptn. of proteins S7, and ZNF7, and L7 from a cell lysate with an anti-L7 antibody. We also show that ZNF7-like L7 and S7 can exist in a ribosome-bound form. This study provides further evidence suggesting that L7 is involved in translational regulation through interactions with components of the translational apparatus

L13 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:435461 HCAPLUS
DOCUMENT NUMBER: 127:187212
TITLE: A novel SR-related protein specifically interacts with the carboxy-terminal domain (CTD) of RNA polymerase II through a conserved interaction domain
AUTHOR(S): Tanner, Stefan; Stagljar, Igor; Georgiev, Oleg; Schaffner, Walter; Bourquin, Jean Pierre
CORPORATE SOURCE: Institut Molekularbiologie, Universitat Zurich, Zurich, CH-8057, Switz.
SOURCE: Biological Chemistry (1997), 378(6), 565-571
CODEN: BICHF3; ISSN: 1431-6730
PUBLISHER: de Gruyter
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The largest subunit of the RNA polymerase II (pol II) contains at the carboxy-terminus a peculiar repetitive sequence that consists of 52 tandem repeats of the consensus motif Tyr-Ser-Pro-Thr-Ser-Pro-Ser, referred to as the C-terminal domain (CTD). Upon transcriptional initiation/promoter clearance, the CTD becomes extensively phosphorylated and apparently remains so during elongation. While the under-phosphorylated CTD plays a role in transcriptional initiation, recent evidence couples the highly phosphorylated CTD to RNA processing, namely poly-adenylation and splicing. Using a yeast 2-hybrid screen, human **proteins** were **selected** that interact with the CTD of RNA polymerase II. The CTD-GAL **fusion protein** used as a bait is highly phosphorylated in yeast and, accordingly, proteins were not isolated implicated in transcriptional regulation but rather proteins with possible roles in RNA splicing. One major cDNA clone isolated this way encodes SRrp129/CASP11, a protein that contains a conserved CTD-interaction domain at the C-terminus and an internal Ser-Arg rich domain (SR domain). Proteins of the SR family were implicated in RNA splicing, notably in the regulation of alternative splicing. It was considered that SRrp129 is an auxiliary splice factor. The method was improved to quickly map domains involved in protein-protein interaction (Stagljar et al., 1996, BioTechniques 21, 430-432). Instead of using sonication for the production of a random DNA fragment library, it was taken advantage of the fact that DNAse I in the presence of manganese (II) produces double strand rather than single strand DNA breaks. The DNA fragment library of the SRrp129 clone was then used in the yeast 2-hybrid system to identify the 100-amino acid domain that interacts with the CTD of RNA polymerase II.

L13 ANSWER 15 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:22559 HCAPLUS
DOCUMENT NUMBER: 126:56580
TITLE: **Transcription activation** by the bacteriophage Mu Mor protein requires the C-terminal

regions of both α and σ70 subunits of Escherichia coli RNA polymerase
AUTHOR(S): Artsimovitch, Irina; Murakami, Katsuhiko; Ishihama, Akira; Howe, Martha M.
CORPORATE SOURCE: Dep. Microbiol. Immunol., Univ. Tennessee, Memphis, TN, 38163, USA
SOURCE: Journal of Biological Chemistry (1996), 271(50), 32343-32348
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Middle transcription of bacteriophage Mu requires Escherichia coli RNA polymerase and a Mu-encoded protein, Mor. Consistent with these requirements, the middle promoter, Pm, has a -10 hexamer but lacks a recognizable -35 hexamer. Interactions between Mor and RNA polymerase were studied using in vitro transcription, DNase I footprinting, and the yeast interaction trap system. The authors observed reduced promoter activity in vitro using reconstituted RNA polymerases with C-terminal deletions in α or σ70. As predicted if α were binding to Pm, the authors detected a polymerase-dependent footprint in the -60 region. Reconstituted RNA polymerases containing Ala substitutions in the α C-terminal domain were used to assay Mor-dependent transcription from Pm in vitro. The D258A substitution and α deletion gave large redns. in activation, whereas the L262A, R265A, and N268A substitutions caused smaller redns. The **interaction trap assay** revealed weak interactions between Mor and both α and σ70; consistent with a key role of α-D258, the D258A substitution abolished interaction, whereas the R265A substitution did not. The authors propose that: (i)α-D258 is a Mor "contact site"; and (ii) residues Leu-262, Arg-265, and Asn-268 indirectly affect Mor-polymerase interaction by stabilizing the ternary complex via α-DNA contact.
REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 16 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:607488 HCAPLUS
DOCUMENT NUMBER: 125:240217
TITLE: Methods of selecting a random peptide that binds to a target protein and HIV-1 Rev-binding protein RIP and its use in diagnosis and therapy
INVENTOR(S): Fritz, Christian C.; Green, Michael R.
PATENT ASSIGNEE(S): University of Massachusetts Medical Center, USA
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9623899	A1	19960808	WO 1995-US9589	19950727

W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT,

LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

AU 9532048	A1	19960821	AU 1995-32048	19950727
PRIORITY APPLN. INFO.:			US 1995-381800	19950201
			WO 1995-US9589	19950727

AB A method of isolating a random peptide-scaffold peptide **fusion protein** that binds a predetd. target protein is disclosed. First, a library of nucleotide sequences encoding random amino acid sequences is **generated** and cloned into a first expression vector to make a library test vector. The nucleotide sequence is expressed within a yeast cell as a test **fusion protein** containing a **transcriptional activation** domain, a random peptide domain, and a scaffold peptide domain. The DNA sequence encoding a target protein cloned into a second expression vector provides a target vector. The expressed target **fusion protein** contains a DNA-binding domain and a target protein. Test **fusion protein**-target **fusion protein** interaction is detected according to a two-hybrid protein-protein interaction assay. Also disclosed are an HIV-1 Rev protein binding peptide isolated by the method of the invention and methods of using the Rev interacting protein. The Rev-binding protein, called RIP (Rev Interacting Protein), is encoded by a DNA fragment from the antisense strand of the human MCM2 homolog. RIP consists of protein encoded by the antisense MCM2 DNA, a peptide derived from the polylinker, and a scaffold protein derived from the Adh C-terminus. The latter scaffold protein is necessary to stabilize the active conformation of the Rev-binding protein. When produced in HIV-1-producing T cell lines, RIP inhibited virion production in a dose-dependent manner.

L13 ANSWER 17 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	1996:575724 HCAPLUS
DOCUMENT NUMBER:	125:239381
TITLE:	The yeast two-hybrid system: forward and reverse
AUTHOR(S):	White, Miachael A.
CORPORATE SOURCE:	Dep. Cell Biol. Neuroscience, Univ. Texas Southwestern Medical Center, Dallas, TX, 75235-9039, USA
SOURCE:	Proceedings of the National Academy of Sciences of the United States of America (1996), 93(19), 10001-10003 CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER:	National Academy of Sciences
DOCUMENT TYPE:	Journal; General Review
LANGUAGE:	English

AB A review, with 12 refs., on reverse 2-hybrid reporter systems to select for mutations in which protein-protein interactions are hindered, with a toxic product forming when the protein-protein interactions occurs. Each protein in the interaction is fused with domains used to establish the reporting function in yeasts. Forward 2-hybrid systems, where reporters expressed are not lethal, may give false positives.

L13 ANSWER 18 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	1996:551368 HCAPLUS
DOCUMENT NUMBER:	125:214277
TITLE:	Method for identifying RXR-interacting proteins (RIP's) and sequences of RIP's and RIP cDNA's
INVENTOR(S):	Moore, David; Seol, Wongi; Choi, Hueng-Sik
PATENT ASSIGNEE(S):	General Hospital Corporation, USA
SOURCE:	PCT Int. Appl., 79 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent
LANGUAGE:	English

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9621677	A1	19960718	WO 1995-US16311	19951208
W: JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5932699	A	19990803	US 1995-372652	19950113
EP 801657	A1	19971022	EP 1995-943114	19951208
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE				

PRIORITY APPLN. INFO.: US 1995-372652 19950113
WO 1995-US16311 19951208

AB Disclosed is a method for determining whether a test protein, is capable of interacting with a retinoid X receptor protein. The method involves: (a) providing a host cell which contains (i) a reporter **gene** operably linked to a protein binding site; (ii) a first fusion **gene** which expresses a first **fusion protein**, the first **fusion protein** including a retinoid X receptor protein covalently bonded to a binding moiety which is capable of specifically binding to the protein binding site; and (iii) a second fusion **gene** which expresses a second **fusion protein**, the second **fusion protein** including the test protein covalently bonded to a **gene** activating moiety; and (b) determining whether the test protein increases expression of the reporter **gene** as an indication of its ability to interact with the retinoid X receptor protein. Also disclosed is purified **DNA** encoding retinoid X receptor-interacting proteins (RIP's) and the polypeptides expressed from such **DNA**. The interaction trap technique was used to isolate cDNA's encoding proteins that interact with the ligand-binding domain of human RXRα. Two clones, RIP14 and RIP 15, were previously undescribed orphan members of the nuclear receptor superfamily while two others showed no significant similarity to any known protein and are candidate **transcriptional coactivators**. Expression of RIP **genes** in various tissues, binding of the RIP's to other receptors and binding to **DNA** was examined RIP14 and RIP15 bound to an overlapping set of specific elements (e.g EcRE and βRARE) as **heterodimers** with RXRα.

L13 ANSWER 19 OF 19 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:623606 HCAPLUS
DOCUMENT NUMBER: 121:223606
TITLE: Nuclear localization of P185NEU tyrosine kinase and its association with **transcriptional transactivation**
AUTHOR(S): Xie, Youming; Hung, Mien-Chie
CORPORATE SOURCE: M. D. Anderson Cancer Center, University of Texas, Houston, TX, 77030, USA
SOURCE: Biochemical and Biophysical Research Communications (1994), 203(3), 1589-98
CODEN: BBRCA9; ISSN: 0006-291X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The rat neu **protooncogene** encodes a 185 kD transmembrane protein (p185neu), which is a member of the epidermal growth factor receptor (EGFr) family. In searching for the signaling transducer of p185neu by using a **two-hybrid selection** system, we found, surprisingly, that the cytoplasmic domain of p185neu, when fused to the DNA-binding domain of GAL4 (amino acids 1-147), functioned as a **transcriptional activator**. We subsequently observed

nuclear localization of p185neu. Interestingly, nuclear p185neu has a much higher extent of tyrosine phosphorylation than its nonnuclear counterpart. Our results suggest that a transmembrane receptor tyrosine kinase may enter the nucleus and be involved in **transcriptional activation**. This novel finding unveils a clue in the understanding of the mechanism of receptor tyrosine kinase-mediated signal transduction.

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=> d que stat l18
L1           50 SEA FILE=HCAPLUS ABB=ON  ((2 OR TWO?)(W)?HYBRID?(W)?SELECTION?
                OR ?INTERACT?(W)?TRAP?(W)?ASSAY?)
L2           16 SEA FILE=HCAPLUS ABB=ON  L1 AND ?PROTEIN?(3A)(?SELECT? OR
                ?FUSION?)
L3            3 SEA FILE=HCAPLUS ABB=ON  L1 AND ?DIMERIZ?
L4           18 SEA FILE=HCAPLUS ABB=ON  L2 OR L3
L8            8 SEA FILE=HCAPLUS ABB=ON  L1 AND ?TRANSCRIPT?(W)?ACTIVAT?
L9           22 SEA FILE=HCAPLUS ABB=ON  L4 OR L8
L10          18 SEA FILE=HCAPLUS ABB=ON  L9 AND ?GENE?
L11           4 SEA FILE=HCAPLUS ABB=ON  L1 AND ?DIMER?
L12           4 SEA FILE=HCAPLUS ABB=ON  L11 AND (DNA? OR ?GENE?)
L13          19 SEA FILE=HCAPLUS ABB=ON  L10 OR L12
L16          18 SEA FILE=HCAPLUS ABB=ON  L1 AND ?LIBRARY?
L17          26 SEA FILE=HCAPLUS ABB=ON  L13 OR L16
L18           7 SEA FILE=HCAPLUS ABB=ON  L17 NOT L13

=> d ibib abs l18 1-7

L18  ANSWER 1 OF 7  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2003:919986  HCAPLUS
DOCUMENT NUMBER:          140:141676
TITLE:                    Assessing the Plasticity of DNA Target Site
                          Recognition of the PI-SceI Homing Endonuclease Using a
                          Bacterial Two-hybrid
                          Selection System
AUTHOR(S):                Gimble, Frederick S.; Moure, Carmen M.; Posey, Karen
                          L.
CORPORATE SOURCE:         Institute of Biosciences and Technology, Center for
                          Genome Research, Texas A & M University System Health
                          Science Center, Houston, TX, 77030, USA
SOURCE:                   Journal of Molecular Biology (2003), 334(5), 993-1008
                          CODEN: JMOBAK; ISSN: 0022-2836
PUBLISHER:                Elsevier
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB   The PI-SceI protein from Saccharomyces cerevisiae is a member of the
     LAGLIDADG family of homing endonucleases that have been used in genomic
     engineering. To assess the flexibility of the PI-SceI-binding interaction
     and to make progress towards the directed evolution of homing
     endonucleases that cleave specified DNA targets, we applied a two-hybrid
     method to select PI-SceI variants from a randomized expression
     library that bind to different DNA substrates. In particular, the
     codon for Arg94, which is located in the protein splicing domain and makes
     essential contacts to two adjacent base-pairs, and the codons for four
     proximal residues were randomized. There is little conservation of the
     wild-type amino acid residues at the five randomized positions in the
     variants that were selected to bind to the wild-type site, yet one of the
     purified derivs. displays DNA-binding specificity and DNA endonuclease
     activity that is similar to that of the wild-type enzyme. A spectrum of
     DNA-binding behaviors ranging from partial relaxation of specificity to
     marked shifts in target site recognition are present in variants selected
     to bind to sites containing mutations at the two base-pairs. Our results
     illustrate the inherent plasticity of the PI-SceI/DNA interface and
     demonstrate that selection based on DNA binding is an effective means of
     altering the DNA cleavage specificity of homing endonucleases.
     Furthermore, it is apparent that homing endonuclease target specificity
     derives, in part, from constraints on the flexibility of DNA contacts
     imposed by hydrogen bonds to proximal residues.
REFERENCE COUNT:          68    THERE ARE 68 CITED REFERENCES AVAILABLE FOR THIS
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RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:737894 HCAPLUS
DOCUMENT NUMBER: 139:241336
TITLE: Two-hybrid screening using growth inhibition by regulated expression of nuclease genes as reporter system
INVENTOR(S): Henkel, Thomas; Rohrbach, Martin
PATENT ASSIGNEE(S): Medigene A.-G., Germany
SOURCE: PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003076618	A1	20030918	WO 2003-EP2352	20030307
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
DE 10210285	A1	20031113	DE 2002-10210285	20020308

PRIORITY APPLN. INFO.: DE 2002-10210285 A 20020308

AB A method of two-hybrid screening that uses regulated expression of two nuclease genes to inhibit the growth of cells in which interactions take place. The efficiency of selection is increased when two genes for growth inhibiting nucleases (DNases, RNases, or a combination) are induced by the interacting proteins. The genes for one or both of the components may be under control of a regulated promoter allowing selection and establishment of a **library**. Induction of expression leads to slower growth which can be readily detected. The strength of the interaction is also reflected in the effects on growth rates. This system can be adapted to screen for inhibitors of protein-protein interactions and to test the effects of amino acid substitutions on the interaction.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:659359 HCAPLUS
DOCUMENT NUMBER: 137:199920
TITLE: Intracellular single-chain variable fragments directed to the Src homology 2 domains of Syk partially inhibit FcεRI signaling in the RBL-2H3 cell line
AUTHOR(S): Dauvillier, Stephanie; Merida, Peggy; Visintin, Michela; Cattaneo, Antonino; Bonnerot, Christian; Dariavach, Piona
CORPORATE SOURCE: Institut de Genetique Moleculaire de Montpellier, Unite Mixte de Recherche 5535 Centre National de la Recherche Scientifique, Montpellier, 34298, Fr.
SOURCE: Journal of Immunology (2002), 169(5), 2274-2283

CODEN: JOIMA3; ISSN: 0022-1767
PUBLISHER: American Association of Immunologists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Intracellular expression of Ab fragments has been efficiently used to inactivate therapeutic targets, oncogene products, and to induce viral resistance in plants. Ab fragments expressed in the appropriate cell compartment may also help to elucidate the functions of a protein of interest. The authors report in this study the successful targeting of the protein tyrosine kinase Syk in the RBL-2H3 rat basophilic leukemia cell line. The authors isolated from a phage display **library** human single-chain variable fragments (scFv) directed against the portion of Syk containing the Src homol. 2 domains and the linker region that separates them. Among them, two scFv named G4G11 and G4E4 exhibited the best binding to Syk in vivo in a yeast **two-hybrid selection** system. Stable transfectants of RBL-2H3 cells expressing cytosolic G4G11 and G4E4 were established. Immunopptn. expts. showed that intracellular G4G11 and G4E4 bind to Syk, but do not inhibit the activation of Syk following FcεRI aggregation, suggesting that the scFv do not affect the recruitment of Syk to the receptor. Nevertheless, FcεRI-mediated calcium mobilization and the release of inflammatory mediators are inhibited, and are consistent with a defect in Bruton's tyrosine kinase and phospholipase C-γ2 tyrosine phosphorylation and activation. Interestingly, FcεRI-induced mitogen-activated protein kinase phosphorylation is not altered, suggesting that intracellular G4G11 and G4E4 do not prevent the coupling of Syk to the Ras pathway, but they selectively inhibit the pathway involving phospholipase C-γ2 activation.

REFERENCE COUNT: 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:851433 HCAPLUS
DOCUMENT NUMBER: 136:1569
TITLE: **Interaction trap assays** using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions
INVENTOR(S): Joung, J. Keith; Miller, Jeffrey; Pabo, Carl O.
PATENT ASSIGNEE(S): Massachusetts Institute of Technology, USA
SOURCE: PCT Int. Appl., 196 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001088197	A2	20011122	WO 2001-US15718	20010516
WO 2001088197	A3	20031231		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-204509P P 20000516

AB The present invention provides methods and compns. for **interaction trap assays** for detecting protein-protein, protein-DNA, or protein-RNA interactions using prokaryotic or microbial eukaryotic hosts. The methods and compns. of the invention may also be used to identify agents which may agonize or antagonize a protein-protein, protein-DNA, or protein-RNA interaction. In certain embodiments, the interaction trap system of the invention is useful for screening libraries with greater than 107 members. In other embodiments, the interaction trap system of the invention is used in conjunction with flow cytometry. The invention further provides a means for simultaneously screening a target protein or nucleic acid sequence for the ability to interact with two or more test proteins or nucleic acids. In one form, the screening involves the use of a selectable marker allowing screening of large nos. of cells without the need to scan for a colorimetric marker. In a second form, screening of a colorimetric marker is by flow cytometry. Screening of a **library** of 108 members in Escherichia coli for C2H2 zinc finger variants is demonstrated.

L18 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:674145 HCAPLUS
DOCUMENT NUMBER: 132:20600
TITLE: Identification of ribonucleoprotein (RNP)-specific protein interactions using a yeast RNP **interaction trap assay** (RITA)
AUTHOR(S): Bouffard, Pascal; Briere, Francis; Wellinger, Raymund J.; Boire, Gilles
CORPORATE SOURCE: Universite de Sherbrooke, Sherbrooke, QC, J1H 5N4, Can.
SOURCE: BioTechniques (1999), 27(4), 790-794,796
CODEN: BTNQDO; ISSN: 0736-6205
PUBLISHER: Eaton Publishing Co.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We describe an adaptation of the yeast three-hybrid system that allows the reconstitution in vivo of tripartite (protein-RNA-protein) ribonucleoproteins (RNPs). To build and try this system that we called RNP **interaction trap assay** (RITA), we used as a model the autoantigenic Ro RNPs. The hY RNAs bear distinct binding sites for Ro60 and La proteins, and Ro RNPs are thus physiol. tripartite (Ro60/hY RNA/La). Using recombinant La (rLa) and Ro60 (rRo60) proteins and recombinant hY RNAs (rhY) co-expressed in yeast, we found that RNPs made of rRo60/rhY/rLa were readily reassembled. Reconstitution of tripartite RNPs was critically dependent on the presence of an appropriate Ro60 binding site on the recombinant RNA. The RITA assay was further used to detect (rRo60/rhY RNP)-binding proteins from a HeLa cell cDNA **library**, allowing specific identification of La and of a novel Ro RNP-binding protein (RoBPI) in more than 70% of pos. clones. RITA assay may complement already available two- and three-hybrid systems to characterize RNP-binding proteins by allowing the in vivo identification of interactions strictly dependent upon the simultaneous presence of a protein and of its cognate RNA.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:145216 HCAPLUS
DOCUMENT NUMBER: 126:141191
TITLE: Cloning, cDNA sequences, and protein degradation functions of four human E6AP-binding proteins

INVENTOR(S): Beer-romero, Peggy L.; Draetta, Giulio; Rolfe, Mark
PATENT ASSIGNEE(S): Mitotix, Inc., USA
SOURCE: PCT Int. Appl., 83 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9640767	A2	19961219	WO 1996-US9040	19960606
WO 9640767	A3	19970313		
W: AU, CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9661533	A1	19961230	AU 1996-61533	19960606
PRIORITY APPLN. INFO.:			US 1995-484878	19950607
			WO 1996-US9040	19960606

AB Novel protein-protein interactions are discovered in human cells between certain cellular proteins, referred to as "E6AP-binding proteins" or "E6AP-BPs", and the cellular protein E6AP, the latter of which is a component of a ubiquitin-ligase (E3) enzyme. The association of E6AP and the subject E6AP-binding proteins implicates the E6AP-binding proteins in a number of basic cellular functions, such as regulation of gene expression, regulation of the cell-cycle, modification of cell surface receptors, biogenesis of ribosomes, and DNA repair. A yeast **interaction trap assay** for protein-protein interactions was used to isolate cDNA encoding proteins able to bind to E6AP from a WI38 cDNA **library**. Full-length clones for 4 interacting proteins (cln57, cln24, cln25, and cln42) were obtained and sequenced. One of the E6AP-binding proteins shares certain homol. with the papillomavirus E6 protein, which also binds E6AP. The E6AP-BPs cause a reversal of p53 degradation by E6AP.

L18 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:47821 HCAPLUS
DOCUMENT NUMBER: 126:99937
TITLE: Genomic libraries and a host strain designed for highly efficient **two-hybrid selection** in yeast
AUTHOR(S): James, Philip; Halladay, John; Craig, Elizabeth A.
CORPORATE SOURCE: Department Biomolecular Chemistry, University Wisconsin, Madison, WI, 53706, USA
SOURCE: Genetics (1996), 144(4), 1425-1436
CODEN: GENTAE; ISSN: 0016-6731
PUBLISHER: Genetics Society of America
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The two-hybrid system is a powerful technique for detecting protein-protein interactions that utilizes the well-developed mol. genetics of the yeast Saccharomyces cerevisiae. However, the full potential of this technique has not been realized due to limitations imposed by the components available for use in the system. These limitations include unwieldy plasmid vectors, incomplete or poorly designed two-hybrid libraries, and host strains that result in the selection of large nos. of false positives. The authors have used a novel multienzyme approach to generate a set of highly representative genomic libraries from S. cerevisiae. In addition, a unique host strain was created that contains three easily assayed reporter genes, each under the control of a different inducible promoter. This host strain is extremely

sensitive to weak interactions and eliminates nearly all false positives using simple plate assays. Improved vectors were also constructed that simplify the construction of the gene fusions necessary for the two-hybrid system. The authors' anal. indicates that the libraries and host strain provide significant improvements in both the number of interacting clones identified and the efficiency of **two-hybrid selections.**

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                 OR ?INTERACT?(W)?TRAP?(W)?ASSAY?)
L2            16 SEA FILE=HCAPLUS ABB=ON  L1 AND ?PROTEIN?(3A)(?SELECT? OR
                 ?FUSION?)
L3             3 SEA FILE=HCAPLUS ABB=ON  L1 AND ?DIMERIZ?
L4            18 SEA FILE=HCAPLUS ABB=ON  L2 OR L3
L8             8 SEA FILE=HCAPLUS ABB=ON  L1 AND ?TRANSCRIPT?(W)?ACTIVAT?
L9            22 SEA FILE=HCAPLUS ABB=ON  L4 OR L8
L10           18 SEA FILE=HCAPLUS ABB=ON  L9 AND ?GENE?
L11            4 SEA FILE=HCAPLUS ABB=ON  L1 AND ?DIMER?
L12            4 SEA FILE=HCAPLUS ABB=ON  L11 AND (DNA? OR ?GENE?)
L13           19 SEA FILE=HCAPLUS ABB=ON  L10 OR L12
L14           43 SEA L13
L15           26 DUP REMOV L14 (17 DUPLICATES REMOVED)

=> d ibib abs l15 1-26

L15  ANSWER 1 OF 26  WPIDS  COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER:      2002-195965 [25]   WPIDS
CROSS REFERENCE:       2002-188750 [24]
DOC. NO. NON-CPI:      N2002-148829
DOC. NO. CPI:          C2002-060636
TITLE:                 Novel purified human metalloproteinase-disintegrin
                       polypeptide, useful for treating ocular and inflammatory
                       disorders, osteoporosis, cancer, restenosis, thrombosis,
                       and chronic pain conditions.
DERWENT CLASS:         B04 D16 S03 T01
INVENTOR(S):           BLACK, R A; DUBOSE, R F; WILEY, S R
PATENT ASSIGNEE(S):    (IMMV) IMMUNEX CORP
COUNTRY COUNT:         97
PATENT INFORMATION:

     PATENT NO        KIND DATE     WEEK      LA   PG
     ---------------------------------------------
     WO 2002010406    A2 20020207 (200225)* EN  101
        RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
            NL OA PT SD SE SL SZ TR TZ UG ZW
         W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
            DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
            KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU
            SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
     AU 2001079060    A  20020213 (200238)
     EP 1307568       A2 20030507 (200332)  EN
         R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
            RO SE SI TR
     JP 2004507234    W  20040311 (200419)      165

APPLICATION DETAILS:

     PATENT NO       KIND                    APPLICATION          DATE
     ---------------------------------------------------------------------
     WO 2002010406   A2                      WO 2001-US23734      20010727
     AU 2001079060   A                       AU 2001-79060        20010727
     EP 1307568      A2                      EP 2001-957300       20010727
                                             WO 2001-US23734      20010727
     JP 2004507234   W                       WO 2001-US23734      20010727
                                             JP 2002-516322       20010727

FILING DETAILS:
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PATENT NO	KIND	PATENT NO
AU 2001079060	A Based on	WO 2002010406
EP 1307568	A2 Based on	WO 2002010406
JP 2004507234	W Based on	WO 2002010406

PRIORITY APPLN. INFO: US 2000-221838P 20000728
AN 2002-195965 [25] WPIDS
CR 2002-188750 [24]
AB WO 200210406 A UPAB: 20040318

NOVELTY - A purified human metalloproteinase-disintegrin (MPD) polypeptide (I) comprising one of 23 31-812 residue amino acid (a.a) sequences, all fully defined in the specification, or its fragments, is new.

DETAILED DESCRIPTION - A purified human metalloproteinase-disintegrin (MPD) polypeptide (I) selected from a polypeptide comprising a 150, 686, 149, 559, 366, 94, 751, 127, 122, 67, 660, 31, 60, 112, 57, 168, 812, 39, 253, 435, 811, 383, or 574 a.a sequence (S1), fully defined in the specification, fragments of the 149, 366, 660, or 435 a.a sequence having disintegrin activity, fragments of the 435 a.a sequence having metalloproteinase activity, residues 43-148 of the 149 a.a sequence, residues 1-366 or 38-366 of the 366 a.a sequence, residues 1-622, 84-622, or 299-633 of the 660 a.a sequence, residues 1-701 of the 812 a.a sequence, residues 1-277 or 278-435 of the 435 a.a sequence, residues 1-322 or 1-627 of the 811 a.a sequence, residues 1-215, 118-215 or 224-383 of the 383 a.a sequence, and residues 29-574 of the 574 a.a sequence.

INDEPENDENT CLAIMS are also included for the following:

(1) a purified polypeptide (II) comprising at least 97 % homology to (S1), where the polypeptide has metalloproteinase or disintegrin activity;

(2) an isolated polynucleotide (III) encoding (I);

(3) an expression vector (IV) comprising (III);

(4) a recombinant host cell (V) comprising (III);

(5) producing (I), comprising culturing (V) under expression conditions, and recovering the polypeptide;

(6) a polypeptide produced by culturing (V) under conditions to promote expression of the polypeptide;

(7) a purified antibody (VI) that specifically binds to (I);

(8) designing (M) an inhibitor or binding agent of (I); and

(9) a system (VII) for analyzing polypeptides or polynucleotides comprises a data set representing a set of one or more of (I), a computer, and a computer algorithm in an executable format on the computer for analyzing the polypeptides.

ACTIVITY - Cytostatic; Antiinflammatory; Osteopathic; Vasotropic; Thrombolytic; Vulnerary; Antiallergic; Antibacterial; Virucide; Protozoacide; Cardiant; Antianemic; Analgesic.

No biological data is given.

MECHANISM OF ACTION - Modulator of **angiogenesis**, endothelial cell migration; modulator of binding of an integrin to ligand (claimed); modulator of biological activity of (I); **gene** therapy.

USE - (I) is useful for identifying an agent that modulates an activity of (I), for modulating **angiogenesis** in a cell or mammal, for modulating endothelial cell migration, and for inhibiting the binding of an integrin to a ligand in a cell or mammal that expresses the integrin, where the mammal is afflicted with a condition such as ocular disorders, malignant and metastatic conditions, inflammatory diseases, osteoporosis and other conditions mediated by accelerated bone resorption, restenosis, inappropriate platelet activation, recruitment, or aggregation, thrombosis, and a condition requiring tissue repair or wound healing (claimed). (I) is useful for treating and diagnosing

integrin-associated or metalloproteinase-associated diseases, in the development of diagnostic and related therapeutics, to identify agents that modulate activity of (I), as diagnostic reagents, as research reagents for investigation of integrin polypeptides and fertilization processes, purification and processing of integrins and/or endothelial cells or T-cells, as a carrier/targeting polypeptide to deliver therapeutic agents to cells, as an immunogen for producing (VI), in a variety of assays to identify binding partners or non-binding-partner molecules or substances, in **interaction trap assays**, as polypeptide purification reagents, as molecular weight and isoelectric focussing markers, as controls for peptide fragmentation, for identification of unknown polypeptides, and for modulating biological activity of polypeptide. (I) or (VI) is useful for treating medical conditions and diseases associated with cell-cell and cell matrix interactions, endothelial migration, **angiogenesis**, inflammation, cancer, allergy, reproductive, neurological and vascular conditions, bacterial, viral or protozoal infections, cardiovascular disorders such as myocardial infarction, chronic pain conditions, endocrine system disorders, gastrointestinal system disorders, genitourinary system disorders, anemia, hematological disorders, cell proliferative disorders, solid tumors, and lymphoproliferative disorders. (III) is useful for numerous diagnostic purposes, as markers for tissues in which a corresponding polypeptide is preferentially expressed, as molecular weight markers, as chromosome markers or tags, to compare with endogenous **DNA** sequences in subjects to identify potential **genetic** disorders, as probes or primers, as an antigen to raise anti-**DNA** antibodies or elicit another immune response, for **gene** therapy, and in chromosome mapping. (VI) is useful for purifying (I), to inhibit the activity of (I), and as agonists.
Dwg.0/1

L15 ANSWER 2 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-188750 [24] WPIDS
CROSS REFERENCE: 2002-195965 [25]
DOC. NO. NON-CPI: N2002-143063
DOC. NO. CPI: C2002-058411
TITLE: Novel substantially purified human polypeptide having homology to A Disintegrin and Metalloproteinase domain (ADAM) polypeptide family, termed ADAM-H9, for treating ocular and inflammatory diseases, osteoporosis, cancer.
DERWENT CLASS: B04 D16 S03 T01
INVENTOR(S): BLACK, R A; DUBOSE, R F; MOSLEY, B A; POINDEXTER, K; WILEY, S R; POINDEXTER, K M
PATENT ASSIGNEE(S): (IMMV) IMMUNEX CORP; (BLAC-I) BLACK R A; (DUBO-I) DUBOSE R F; (MOSL-I) MOSLEY B A; (POIN-I) POINDEXTER K M; (WILE-I) WILEY S R
COUNTRY COUNT: 97
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002010405	A2	20020207	(200224)*	EN	72
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2001080843	A	20020213	(200238)		
EP 1305434	A2	20030502	(200331)	EN	

R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
JP 2004504845 W 20040219 (200414) 136
US 2004047854 A1 20040311 (200419)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002010405	A2	WO 2001-US23709	20010727
AU 2001080843	A	AU 2001-80843	20010727
EP 1305434	A2	EP 2001-959270	20010727
		WO 2001-US23709	20010727
JP 2004504845	W	WO 2001-US23709	20010727
		JP 2002-516321	20010727
US 2004047854	A1	WO 2001-US23709	20010727
		US 2003-343063	20030610

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2001080843	A Based on	WO 2002010405
EP 1305434	A2 Based on	WO 2002010405
JP 2004504845	W Based on	WO 2002010405

PRIORITY APPLN. INFO: US 2001-282550P 20010409; US 2000-221838P 20000728; US 2003-343063 20030610

AN 2002-188750 [24] WPIDS
CR 2002-195965 [25]
AB WO 200210405 A UPAB: 20040318
NOVELTY - A substantially purified human polypeptide (I) having homology to A Disintegrin And Metalloproteinase domain (ADAM) polypeptide family, termed ADAM-H9, comprising a sequence of 66, 51, 96, 466, 352, 329 or 542 amino acids fully defined in the specification, and its fragments or variants, is new.

DETAILED DESCRIPTION - A substantially purified human polypeptide (I) having homology to A Disintegrin And Metalloproteinase domain (ADAM) polypeptide family, termed ADAM-H9, comprising a sequence of 66, 51, 96, 466, 352, 329 or 542 amino acids fully defined in the specification, and its fragments or variants, is new.

(I) is selected from:

(a) a polypeptide comprising a sequence (S1) of 66 (N1), 51 (N2), 96 (N3), 466 (N4), 352 (N5) or 329 (N6) amino acids fully defined in the specification;

(b) fragments or soluble fragments of (S) having disintegrin activity;

(c) fragments of (S) comprising at least 20-30 contiguous amino acids or comprising a disintegrin domain sequence;

(d) amino acid residues 73 to residues between 360 and 362 of the N4;

(e) amino acid residues between 1 and 16 to residues between 285 and 287 of N5;

(f) amino acid residues between 1 and 73 to residues between 314 and 329 of N6;

(g) amino acid sequences comprising at least 10 contiguous amino acids and sharing amino acid identity with the above mentioned sequences, where the percent identity is selected from at least 85%, preferably at least 99.5%; and

(h) a polypeptide comprising a sequence of 542 amino acids fully

defined in the specification.

INDEPENDENT CLAIMS are also included for the following:

(1) a soluble polypeptide (II) having disintegrin activity linked to a second polypeptide such as leucine zipper polypeptide, an Fc polypeptide, or a peptide linker;

(2) an isolated polynucleotide (III) encoding (I) or (II);

(3) an isolated polynucleotide (IV) comprising (III) operably linked to a polynucleotide encoding a polypeptide of interest;

(4) an expression vector (V) comprising (III) or (IV);

(5) a recombinant host cell (VI) comprising (III) or (IV);

(6) production of (I);

(7) a polypeptide produced by culturing (VI);

(8) a substantially purified antibody (VII) that specifically binds to (I);

(9) designing (M) an inhibitor or binding agent of (I), comprising determining the 3-D structure of the polypeptide, analyzing the 3-D structure for binding sites of substrates or ligands, designing a molecule that is predicted to interact with the polypeptide and determining the inhibitory or binding activity of the molecule; and

(10) a system (VIII) for analyzing polypeptides or polynucleotides comprises a data set representing a set of one or more of (I), or one or more of (III), or a combination of polypeptides and polynucleotides, a computer, and a computer algorithm in an executable format on the computer for analyzing the polypeptides or polynucleotides.

ACTIVITY - Cytostatic; antiinflammatory; osteopathic; vasotropic; thrombolytic; vulnerary; antiallergic; antibacterial; virucide; protozoacide; cardiant; antianemic; analgesic; antitumor.

Experimental protocols are given but not results are given.

MECHANISM OF ACTION - Modulator of **angiogenesis**, endothelial cell migration; modulator of binding of an integrin to ligand; inhibitor of biological activity of (I) (claimed); **gene** therapy; antagonist of (I); antagonist of protein processing function of metalloproteinases.

USE - (I) is useful for identifying an agent (an antibody, a small molecule, a peptide or a peptidomimetic) that modulates an activity of (I), for inhibiting **angiogenesis** in a mammal, for modulating **angiogenesis** in a tissue, for modulating endothelial cell migration in vitro or in vivo, for inhibiting the binding of an integrin to a ligand, and for modulating the binding of an integrin to a ligand in a mammal afflicted with a condition such as ocular disorders, malignant and metastatic conditions, inflammatory diseases, osteoporosis, accelerated bone resorption disorders, restenosis, inappropriate platelet activation, recruitment, or aggregation, thrombosis, and a condition requiring tissue repair or wound healing. The (I) used for treating the above conditions is a multimer (a **dimer** or trimer) which comprises an Fc polypeptide, a leucine zipper or a peptide linker. The multimer is a 542 amino acid sequence defined in the specification (claimed).

(I) is useful for treating disintegrin-associated disorder and conditions, to identify agents that modulate activity of (I), as diagnostic reagents, as research reagents for investigation of integrin polypeptides and fertilization processes, purification and processing of integrins and/or endothelial cells or T-cells, as a carrier/targeting polypeptide to deliver therapeutic agents to cells, as an immunogen for producing (VII), in a variety of assays to identify binding partners or non-binding-partner molecules or substances of (I), in **interaction trap assays**, as polypeptide purification reagents, and for purifying or identifying cells that express a binding partner on the cell surface.

(I) or (VII) is useful for treating medical conditions and diseases

associated with cell-cell and cell matrix interactions, endothelial migration, **angiogenesis**, inflammation, allergy, reproductive, neurological and vascular conditions, bacterial, viral or protozoal infections, cardiovascular disorders such as myocardial infarction, chronic pain conditions, endocrine system disorders, gastrointestinal system disorders, genitourinary system disorders, anemia, hematological disorders, and oncologic conditions such as cancer.

(II) is useful for numerous diagnostic purposes, as markers for tissues in which a corresponding polypeptide is preferentially expressed, as molecular weight markers, as chromosome markers or tags, to compare with endogenous **DNA** sequences in subjects to identify potential **genetic** disorders, as probes or primers, as an antigen to raise anti-**DNA** antibodies or elicit another immune response, for **gene** therapy, in chromosome mapping, to analyze abnormalities associated with a **gene** corresponding to (I), and as a positional markers to map other **genes** of unknown location. (VII) is useful for purifying (I), to inhibit the activity of (I), and as agonists. Dwg.0/3

L15 ANSWER 3 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-255941 [30] WPIDS
DOC. NO. CPI: C2002-076291
TITLE: New isolated and/or recombinant ubiquitin ligase such as SIP (SKP Interacting Protein) ligase, for treating diseases associated with aberrant protein degradation, cell proliferation, differentiation, and cell survival.
DERWENT CLASS: B04 D16
INVENTOR(S): CALIGIURI, M; ROLFE, M
PATENT ASSIGNEE(S): (CALI-I) CALIGIURI M; (ROLF-I) ROLFE M
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2002025569	A1	20020228 (200230)*			44

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2002025569	A1	US 1997-915048	19970820

PRIORITY APPLN. INFO: US 1997-915048 19970820
AN 2002-255941 [30] WPIDS
AB US2002025569 A UPAB: 20020513
NOVELTY - An isolated and/or recombinant ubiquitin ligase (I), such as SIP (SKP Interacting Protein) ligase, for example isolated and/or recombinant cdc4 polypeptide comprising a sequence identical or homologous to a sequence (S1) comprising 1121 or 162 amino acids, given in the specification, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an isolated nucleic acid (II) comprising a sequence encoding a cdc4 polypeptide or its portion, or a complement or (II);

(2) an isolated nucleic acid (III) comprising a sequence encoding a vertebrate SIP polypeptide;

(3) an expression vector (IV) capable of replicating in a prokaryotic or eukaryotic cell comprising (IV);

(4) a host cell (V) transfected with (IV) and expressing (I);

(5) production of (I);

(6) a transgenic animal (VI) having cells which harbor a **transgene** comprising (II) or (III), or in which a **gene** comprising (II) or (III) is disrupted;

(7) an isolated nucleic acid (VII) which selectively hybridizes under high stringency conditions to at least 10 nucleotides of a sequence (S2) comprising 3363 or 484 base pairs, given in the specification, or its complement, where (VII) can specifically detect or amplify a sequence of a vertebrate cdc4 **gene**;

(8) a reconstituted protein mixture (VIII) comprising an SIP polypeptide and a cell-cycle regulatory protein;

(9) an isolated SIP polypeptide (IX) having a ubiquitin group attached to cysteine;

(10) an assay (M1) for identifying an inhibitor of an SIP-mediated ubiquitination;

(11) an assay (M2) for identifying an inhibitor of an interaction between a substrate polypeptide and a SIP protein;

(12) diagnosing (M3) a hyperproliferative disorder in a patient where the disorder is associated with the destabilization of a CKI protein in cells of the patient, by ascertaining the level of expression of a SIP ligase in a sample of cells from the patient, and diagnosing the presence or absence of hyperproliferative disorder utilizing, at least in part, the ascertained level expression or activity of the ligase, where an increase level of a SIP protein or SIP ligase activity in the sample, relative to a normal control sample of cells, correlates with the presence of a hyperproliferative disorder; and

(13) a prognostic method (M4) for evaluating the aggressiveness and/or rate of recurrence of a disorder marked by aberrant hyperproliferation, aberrant dedifferentiation and/or aberrant apoptosis of cells, by ascertaining the level of SIP ligase expression and/or SIP ligase activity in a sample of cells from a patient, and ascertaining the aggressiveness and/or risk for recurrence of the disorder, at enzymatic activity, where an increased level in the sample, relative to a normal control sample of cells, correlates with a more aggressive form of the disorder and an increased risk of recurrence of the disorder.

ACTIVITY - Cytostatic; antipsoriatic; antiarteriosclerotic; antiinflammatory.

MECHANISM OF ACTION - Cell proliferation, differentiation, and/or survival modulator; cell-cycle of an eukaryotic cell regulator; entry of a mammalian or yeast cell into S phase modulator; wild-type form of SIP protein agonist/antagonist; **gene** therapy; antisense therapy. No biological data is given.

USE - (I) is useful for modulating cell proliferation, differentiation, and/or survival, and for treating diseases or conditions associated with aberrant protein degradation, cell proliferation, differentiation and/or cell survival, where the diseases are selected from cancer, leukemia, psoriasis, bone diseases, proliferative disorders such as involving connective tissues, atherosclerosis, and other smooth muscle proliferative disorder, and chronic inflammation. (I) is useful for mediating and/or catalyzing the transfer of a ubiquitin molecule from a relevant ubiquitin conjugating enzyme (UBC) to a lysine residue of its substrate protein, for regulating the cell-cycle of an eukaryotic cell, for modulating proliferation/cell growth of a eukaryotic cell, for modulating entry of a mammalian or yeast cell into S phase, for ubiquitination of a cell-cycle regulator, e.g., a cyclin dependent kinase inhibitor, e.g., p27, for modulating differentiation of cells/tissue, for modulating cell growth or proliferation by influencing the action of other cellular proteins, as a specific agonist of the function of the wild-type form of the protein, or as a specific antagonist, such as a catalytically inactive mutant. (I) is useful for **generating** an

interaction trap assay and subsequently detecting agents with disrupt binding of the proteins. A nucleic acid (II) encoding (I) is useful for **generating** expression constructs and in antisense therapy.
Dwg.0/2

L15 ANSWER 4 OF 26 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2002709162 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12364328
TITLE: Multimerization of the protein-tyrosine phosphatase (PTP)-like insulin-dependent diabetes mellitus autoantigens IA-2 and IA-2beta with receptor PTPs (RPTPs). Inhibition of RPTPalpha enzymatic activity.
AUTHOR: Gross Steffen; Blanchetot Christophe; Schepens Jan; Albet Sabrina; Lammers Reiner; den Hertog Jeroen; Hendriks Wiljan
CORPORATE SOURCE: Department of Cell Biology, Nijmegen Center for Molecular Life Sciences, University of Nijmegen, The Netherlands.
SOURCE: Journal of biological chemistry, (2002 Dec 13) 277 (50) 48139-45.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200301
ENTRY DATE: Entered STN: 20021217
Last Updated on STN: 20030129
Entered Medline: 20030128

AB Most receptor-type protein-tyrosine phosphatases (RPTPs) contain two tandem PTP domains. For some RPTPs the enzymatically inactive membrane-distal phosphatase domains (D2) were found to bind enzymatically active membrane proximal PTP (D1) domains, and oligomerization has been proposed as a **general** regulatory mechanism. The RPTP-like proteins IA-2 and IA-2beta, major autoantigens in insulin-dependent diabetes mellitus, contain just a single enzymatically inactive PTP-like domain. Their physiological role is as yet enigmatic. To investigate whether the catalytically inactive cytoplasmic domains of IA-2 and IA-2beta are involved in oligomerization, we exploited **interaction trap assay** in yeast and glutathione S-transferase pull-down and co-immunoprecipitation strategies on lysates of transfected COS-1 cells. The results show that IA-2 and IA-2beta are capable of homo- and **heterodimerization** to which both the juxtamembrane region and the phosphatase-like segment can contribute. Furthermore, they can form **heterodimers** with some other RPTP members, most notably RPTPalpha and RPTPepsilon, and down-regulate RPTPalpha enzymatic activity. Thus, in addition to homo-**dimerization**, the enzymatic activity of receptor-type PTPs can be regulated through **heterodimerization** with other RPTPs, including the catalytically inactive IA-2 and IA-2beta.

L15 ANSWER 5 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-083007 [11] WPIDS
DOC. NO. CPI: C2002-025156
TITLE: **Interaction trap assays** to detect protein-protein, protein-DNA, protein-RNA interaction by using reporter **genes** which upon expression confer growth advantage on host cell or result in detectable fluorescent signal.
DERWENT CLASS: B04 D16
INVENTOR(S): JOUNG, J K; MILLER, J; PABO, C O
PATENT ASSIGNEE(S): (MASI) MASSACHUSETTS INST TECHNOLOGY; (JOUN-I) JOUNG J K;

(MILL-I) MILLER J; (PABO-I) PABO C O
COUNTRY COUNT: 96
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001088197	A2	20011122	(200211)*	EN	196
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW					
AU 2001063155	A	20011126	(200222)		
US 2002119498	A1	20020829	(200259)		
US 2003044787	A1	20030306	(200320)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001088197	A2	WO 2001-US15718	20010516
AU 2001063155	A	AU 2001-63155	20010516
US 2002119498	A1 Provisional	US 2000-204509P	20000516
	CIP of	US 2001-858852	20010516
		US 2001-990762	20011114
US 2003044787	A1 Provisional	US 2000-204509P	20000516
		US 2001-858852	20010516

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001063155	A	Based on	WO 2001088197

PRIORITY APPLN. INFO: US 2000-204509P 20000516; US 2001-858852 20010516; US 2001-990762 20011114

AN 2002-083007 [11] WPIDS

AB WO 200188197 A UPAB: 20020215

NOVELTY - Selecting an interacting pair of test polypeptides, comprising providing a population of prokaryotic cells (H1) which contain a reporter **gene** (R1) operably linked to a transcriptional regulatory sequence (TRS) which includes binding sites (DNA binding domain (DBD) recognition elements) for DBD, and a chimeric **gene** (C1) encoding a **fusion protein** (F1) that includes DBD and test polypeptide, is new.

DETAILED DESCRIPTION - Selecting (M1) an interacting pair of test polypeptides, comprising providing a population of prokaryotic cells (H1) which contain a reporter **gene** (R1) operably linked to a transcriptional regulatory sequence (TRS) which includes binding sites (DNA binding domain (DBD) recognition elements) for DBD, and a chimeric **gene** (C1) encoding a **fusion protein** (F1) that includes DBD and test polypeptide, is new. The cells also contain a second chimeric **gene** (C2) which encodes a second **fusion protein** (F2) that includes an activation tag and second test polypeptide. Interaction of (F1) and (F2) in the host cell results in a desired level of expression of the reporter **gene** that confers a growth advantage on the host cell, or results in the signal detectable by fluorescence activated cell sorting (FACS). The host cells with a growth

advantage are isolated or growth cells are isolated based on desired level of expression of reporter **gene** using FACS. The cells comprise (F1) and (F2) which interact, thus selecting an interacting pair of test polypeptides. (F1) and/or (F2) are a part of a library of at least 107 members, such that at least 107 unique pairs of test polypeptides could be tested for interaction.

INDEPENDENT CLAIMS are also included for the following:

(1) detecting (M2) an interaction between a test polypeptide and DNA sequence, comprising:

(a) providing a population of prokaryotic host cells (H2) each of which contains (R1) operably linked to TRS, and a chimeric **gene** (C3) which encodes a **fusion protein** (F3) that includes a test polypeptide and an activation tag, where interaction between test polypeptide of (F3) and DRE in a host cell results in a desired level of expression of (R1) that confers a growth advantage on the host cell, or results in signal detectable by FACS; and

(b) isolating host cells with growth advantage, or based on desired level of expression of (I) using FACS, comprising a (F3) that interact with DBD based recognition element;

(2) selecting (M4) a polypeptide which differentially interacts with at least two different test polypeptides, comprising:

(a) providing a population of prokaryotic host cells (H4), where each cell contains (R1) operably linked to TRS, a second reporter **gene** (I) operably linked to TRS which includes binding sites (DRE) for a second DNA-binding domain, a first chimeric **gene** which encodes a **fusion protein** (FP1) including a first DNA-binding domain and first test polypeptide, a second chimeric **gene** which encodes a second **fusion protein** (FP2) including a second DNA-binding domain and a second test polypeptide, a third chimeric **gene** which encodes a third **fusion protein** (FP3) including an activation tag and third test polypeptide, where the FP3 is part of a library of at least 107 members; and

(b) interaction of FP1 and FP3 in the host cell results in expression of the (R1) and resulting in signal detectable by FACS, interaction of (F2) and (F3) in the host cell results in expression of (I) and resulting in signal detectable by FACS and isolating host cells comprising FP3 capable of interacting with FP1, the FP2, or the FP1 and FP2 based on a desired level of expression of the (R1), (I), or (R1) or (I), respectively;

(3) selecting (M5) a polypeptide that differentially interacts with at least two different DNA sequences, comprising:

(a) providing a population of prokaryotic host cells (H5) each of which contains (R1), (I) and a chimeric **gene** which encodes a **fusion protein** including a test polypeptide and an activation tag, where a **fusion protein** is part of a library of at least 107 members, interaction of a **fusion protein** with the first, second DRE in the host cells results in expression of (R1) and (I), respectively; and

(b) isolating the host cells comprising a **fusion protein** that interacts with the first DRE and/or the second DRE based on a desired level of expression of (R1) and/or (I), respectively;

(4) a polypeptide (II) isolated by (M2);

(5) a binding site (III) isolated by (M2);

(6) an interacting pair (IV) of (II) and (III);

(7) a kit (K1) for selecting a polypeptide that interacts with a test polypeptide;

(8) a kit (K2) for detecting an interaction between a test DNA-binding domain polypeptide and a DNA sequence;

(9) a test polypeptide isolated using (K1);

(10) a test DNA-binding domain (V) isolated using (K2);

(11) a binding site (VI) for DNA isolated using (K2); and
(12) an interacting pair of (V) and (VI).

USE - For detecting protein-protein, protein-DNA, protein-RNA interaction. (M1) and (M2) are useful for selecting test agents that modulate protein-protein interaction or protein-DNA interaction, respectively. The method involves providing (H1) and (H2), where the host cell is an imp- or gram positive strain of bacteria, contacting host cell with test agent and identifying agents which modulate expression of reporter **gene**. The test agent is a peptide, nucleic acid, carbohydrate, natural product extract library or small organic molecule. (M4) and (M5) are useful for selecting test agents that differentially modulate the interaction of a polypeptide with at least two different test polypeptides or selecting a test agent that differentially modulates the interaction of the polypeptide with at least two different DNA sequences, respectively. (All claimed).

ADVANTAGE - Use of reporter **genes** which conferred selective growth traits allows the use of libraries large enough to significantly improve the chance of finding interacting partners.
Dwg.0/9

L15 ANSWER 6 OF 26 MEDLINE on STN
ACCESSION NUMBER: 2001257276 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11148140
TITLE: Tara, a novel F-actin binding protein, associates with the Trio guanine nucleotide exchange factor and regulates actin cytoskeletal organization.
AUTHOR: Seipel K; O'Brien S P; Iannotti E; Medley Q G; Streuli M
CORPORATE SOURCE: Department of Cancer Immunology and AIDS, Dana-Farber Cancer Institute, Boston, MA 02115, USA.
CONTRACT NUMBER: CA55547 (NCI)
CA75091 (NCI)
SOURCE: Journal of cell science, (2001 Jan) 114 (Pt 2) 389-99.
Journal code: 0052457. ISSN: 0021-9533.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF281030
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010521
Last Updated on STN: 20010521
Entered Medline: 20010517

AB Reorganization of the actin cytoskeleton is essential to numerous cellular processes including cell locomotion and cytokinesis. This actin remodeling is regulated in part by Rho family GTPases. Previous studies implicated Trio, a Dbl-homology guanine nucleotide exchange factor with two exchange factor domains, in regulating actin cytoskeleton reorganization, cell motility and cell growth via activation of Rho GTPases. Trio is essential for mouse embryonic development and Trio-deficiency is associated with abnormal skeletal muscle and neural tissue development. Furthermore, **genetic** analyses in Caenorhabditis elegans and Drosophila demonstrate a role for trio-like **genes** in cell migration and axon guidance. Herein we characterize a novel Trio-binding protein, Tara, that is comprised of an N-terminal pleckstrin homology domain and a C-terminal coiled-coil region. Trio and Tara associate as assessed by the yeast **interaction-trap assays** and mammalian co-immunoprecipitation studies. Ectopically expressed Tara localizes to F-actin in a periodic pattern that is highly similar to the pattern of myosin II. Furthermore, a direct interaction between Tara and F-actin is indicated by in vitro binding studies. Cells

that transiently or stably overexpress Tara display an extensively flattened cell morphology with enhanced stress fibers and cortical F-actin. Tara expression does not alter the ability of the cell to attach or to initially spread, but rather increases cell spreading following these initial events. Tara stabilizes F-actin structures as indicated by the relative resistance of Tara-expressing cells to the F-actin destabilizer Latrunculin B. We propose that Tara regulates actin cytoskeletal organization by directly binding and stabilizing F-actin, and that the localized formation of Tara and Trio complexes functions to coordinate actin remodeling.

L15 ANSWER 7 OF 26 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2001285543 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11233598
TITLE: **Two-hybrid selection** assay to identify **proteins** interacting with polymerase II transcription factors and regulators.
AUTHOR: Petrascheck M; Castagna F; Barberis A
CORPORATE SOURCE: University of Zurich, Switzerland.
SOURCE: BioTechniques, (2001 Feb) 30 (2) 296-8, 300, 302. Journal code: 8306785. ISSN: 0736-6205.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20010529
Entered Medline: 20010524

AB The RNA polymerase III-based two-hybrid system has been developed to detect interactions between proteins such as RNA polymerase II transcription factors and regulators that cannot be studied by the original RNA polymerase II two-hybrid system. This novel method appears to be most useful for a refined analysis of already known protein-protein interactions. However, the application of this system in library screenings has been impaired by the lack of a suitable assay for the selection of the activated pol III reporter **gene** in yeast. Here, we describe a novel selection assay for the pol III-based two-hybrid system that makes it readily usable for screening expression libraries to search for interacting partners. Our system utilizes a temperature-sensitive (ts) U6 snRNA, which is synthesized by RNA polymerase III from a mutated SNR6 **gene** in yeast. In this ts strain, interactions between hybrid proteins activate an artificial pol III reporter construct (UASG-SNR6), which controls expression of wild-type U6 snRNA. This wild-type U6 snRNA can suppress the ts phenotype and allow growth at the nonpermissive temperature of 37 degrees C, thus providing a positive **selection** system for interacting **proteins**.

L15 ANSWER 8 OF 26 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 2002121249 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11842428
TITLE: Identifying and modifying protein-DNA and protein-protein interactions using a bacterial **two-hybrid selection** system.
AUTHOR: Joung J K
CORPORATE SOURCE: Department of Pathology, Division of Molecular Pathology and Research, Massachusetts General Hospital, Charlestown, Massachusetts 02129, USA.. jjoung@partners.org
CONTRACT NUMBER: 1 K08 DK02883-01 (NIDDK)
SOURCE: Journal of cellular biochemistry. Supplement, (2001) Suppl

37 53-7. Ref: 12
Journal code: 8207539. ISSN: 0733-1959.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020222
Last Updated on STN: 20030214
Entered Medline: 20020429

AB A bacterial two-hybrid system based on **transcriptional activation** in E. coli has recently been described. A variety of different protein-DNA and protein-protein interactions from bacteria, yeast, and humans have been studied using this bacterial-based system. The method, because it is based in bacteria, offers significant advantages relative to its yeast counterpart including the ability to analyze complex libraries > 10(8) in size, ease of use, and speed. The ability to easily and rapidly process very large libraries make this system a powerful tool for identifying, modifying, or optimizing protein-DNA and protein-protein interactions.

L15 ANSWER 9 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2000-686012 [67] WPIDS
CROSS REFERENCE: 1998-041296 [04]
DOC. NO. NON-CPI: N2000-507111
DOC. NO. CPI: C2000-208632
TITLE: Set of **DNA** molecules, useful in **interaction trap assays**, encoding **fusion proteins** of candidate interacting protein with **DNA** binding domain or activation domain.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BRENT, R; FINLEY, R L
PATENT ASSIGNEE(S): (GEHO) GEN HOSPITAL CORP
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 6132963	A	20001017	(200067)*		11

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
US 6132963	A	Cont of	US 1994-263566	19940622
		Cont of	US 1997-783534	19970114
			US 1997-949376	19971014

FILING DETAILS:

PATENT NO	KIND		PATENT NO
US 6132963	A	Cont of	US 5695941

PRIORITY APPLN. INFO: US 1994-263566 19940622; US 1997-783534 19970114; US

1997-949376 19971014
AN 2000-686012 [67] WPIDS
CR 1998-041296 [04]
AB US 6132963 A UPAB: 20001223
NOVELTY - Set of **DNA** molecules (I), each encoding a different naturally occurring candidate interacting protein (II) fused to either a **DNA**-binding domain or a weak **gene** activation domain to which it is not naturally bound. The set contains at least 10 (I) and the amino acid sequences of (II) are known.
DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a set of eukaryotic cells containing one of the sets of (I).
USE - (I) are reagents for performing trap interaction assays to determine if two (or more) proteins can interact with each other, also for identification and isolation of the interacting proteins which are potential therapeutic and diagnostic agents (also the **genes** that encode them).
ADVANTAGE - (I) provide rapid and inexpensive assays for identifying interacting proteins or their **genes**. Proteins of widely differing affinities may be detected and inducible promoters may be used, e.g. to allow brief expression of a protein that is toxic when expressed continuously. The use of weak activation domains avoids the limitations imposed by use of strong activation domains and interactions between 3 or more proteins can be detected.
Dwg.0/1

L15 ANSWER 10 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2000-181145 [16] WPIDS
DOC. NO. CPI: C2000-056517
TITLE: Nucleic acid encoding recombinant human cyclin-dependent kinase binding protein (cdc37), used for regulating cell proliferation and differentiation, such as for treating cancer.
DERWENT CLASS: B04 D16
INVENTOR(S): DRAETTA, G; GYURIS, J; LAMPHERE, L
PATENT ASSIGNEE(S): (MITO-N) MITOTIX INC
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 6015692	A	20000118	(200016)*		32

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
US 6015692	A	CIP of	US 1994-253155	19940602
		CIP of	US 1995-466679	19950606
		Cont of	US 1996-625209	19960401
			US 1997-853733	19970509

FILING DETAILS:

PATENT NO	KIND		PATENT NO
US 6015692	A	CIP of	US 5691147
		Cont of	US 5756671

PRIORITY APPLN. INFO: US 1996-625209 19960401; US 1994-253155 19940602; US

1995-466679 19950606; US
1997-853733 19970509

AN 2000-181145 [16] WPIDS

AB US 6015692 A UPAB: 20000330

NOVELTY - Pure nucleic acid (I) encoding a recombinant polypeptide (II) having a cdc37 sequence at least 80% identical with a 378 amino acid (aa) sequence (A), given in the specification, or its fragments, that bind specifically to at least one of cyclin-dependent kinase (CDK) and extracellular signal-regulated kinase (erk).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(a) expression vector, replicable in eukaryotic and/or prokaryotic cells, comprising (I);

(b) host cell transfected with this vector and able to express (II);

(c) recombinant production of (II) by culturing cells of (b);

(d) composition comprising a purified oligonucleotide (ON) containing a region that hybridizes under stringent conditions with at least 50 consecutive nucleotides (nt) of the sense or antisense strands of a sequence (B) of 1599 bp (base pairs) (given in the specification), or its natural mutants;

(e) recombinant transfer system comprising **gene** construct that includes (B), operably linked to a transcriptional regulator and a **gene** delivery component; and

(f) test kit for detecting cells that contain a cdc37 mRNA transcript comprising the composition of (d).

ACTIVITY - Antitumor; growth regulatory; antipsoriatic; antiproliferative; anti-atherosclerotic; anti-inflammatory; antifungal.

No biological data.

MECHANISM OF ACTION - (II) binds to (and modulates) CDK/erk (possibly also p53), so regulates progress through the cell cycle and thus cell growth, differentiation and survival.

USE - (I) is useful:

(i) for producing recombinant (II);

(ii) as source of probes and primers for identifying transformed cells, measuring levels of cdc37-encoding nucleic acid and for detecting mutations or deletions in cdc37 **genes** (for diagnosis of cell proliferative disease or susceptibility);

(iii) in **gene** therapy, e.g. to promote **regeneration** of liver or lung tissue;

(iv) as antisense therapeutics, for treating cancer, leukemia, psoriasis, bone disease, fibroproliferation, atherosclerosis, chronic inflammation etc.; and

(v) for producing transgenic animals that express heterologous cdc37 or have an endogenous cdc37 **gene** deleted.

(II), or its fragments, are useful:

(i) for modulating growth, differentiation and survival of cells, including tumor cells;

(ii) as agonists or antagonists of wild-type cdc37;

(iii) as immunogens for raising specific antibodies (Ab); and

(iv) for screening for agents, potential antimycotics, that act on yeast CDC2/Cdc37 complexes but not on corresponding mammalian complexes.

Antagonists that inhibit interaction of cdc37 with other proteins, e.g. peptidomimetics or mutant forms of cdc37, are used to modulate cell proliferation and/or differentiation. Antibodies are used to screen cDNA expression libraries and as reagents for determination of cdc37 levels in tissues, e.g. for diagnosing cancer.

Dwg.0/1

L15 ANSWER 11 OF 26 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2000319035 MEDLINE

DOCUMENT NUMBER: PubMed ID: 10852947
TITLE: A bacterial **two-hybrid selection** system for studying **protein**-DNA and protein-protein interactions.
AUTHOR: Joung J K; Ramm E I; Pabo C O
CORPORATE SOURCE: Howard Hughes Medical Institute and Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02139, USA.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2000 Jun 20) 97 (13) 7382-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000811
Last Updated on STN: 20000811
Entered Medline: 20000731

AB We have developed a bacterial "two-hybrid" system that readily allows selection from libraries larger than 10(8) in size. Our bacterial system may be used to study either protein-DNA or protein-protein interactions, and it offers a number of potentially significant advantages over existing yeast-based one-hybrid and two-hybrid methods. We tested our system by selecting zinc finger variants (from a large randomized library) that bind tightly and specifically to desired DNA target sites. Our method allows sequence-specific zinc fingers to be isolated in a single selection step, and thus it should be more rapid than phage display strategies that typically require multiple enrichment/amplification cycles. Given the large library sizes our bacterial-based selection system can handle, this method should provide a powerful tool for identifying and optimizing protein-DNA and protein-protein interactions.

L15 ANSWER 12 OF 26 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 2000395089 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10849009
TITLE: The PKC targeting protein RACK1 interacts with the Epstein-Barr virus activator protein BZLF1.
AUTHOR: Baumann M; Gires O; Kolch W; Mischak H; Zeidler R; Pich D; Hammerschmidt W
CORPORATE SOURCE: GSF-National Research Center for Environment and Health, Institute of Clinical Molecular Biology and Tumor Genetics, Department of Gene Vectors, Munchen, Germany.
SOURCE: European journal of biochemistry / FEBS, (2000 Jun) 267 (12) 3891-901. Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000824
Last Updated on STN: 20000824
Entered Medline: 20000817

AB Phorbol esters reactivate Epstein-Barr virus (EBV) from latently infected cells via **transcriptional activation** of the viral immediate-early **gene** BZLF1. BZLF1 is a member of the extended AP-1 family of transcription factors that binds to specific BZLF1-binding motifs within early EBV promoters and to consensus AP-1 sites. Regulation of BZLF1's activity is achieved at the transcriptional level as well as

through post-translational modifications. Recently, we reported that the transcriptional activity of BZLF1 is augmented by TPA [Baumann, M., Mischak, H., Dammeier, S., Kolch, W., Gires, O., Pich, D., Zeidler, R., Delecluse, H. J. & Hammerschmidt, W., (1998) J. Virol. 72, 8105-8114]. The increase of BZLF1's activity depends on a single serine residue (S186) that is phosphorylated by protein kinase C (PKC) in vitro and in vivo after stimulation with 12-O-tetradecanoylphorbol-13-acetate (TPA). Here, we identified RACK1 as a binding partner of BZLF1 in a yeast **interaction trap assay.** RACK stands for receptor of activated C-kinase and is involved in targeting activated PKCs and other signaling proteins. In vivo, RACK1 binds directly to the transactivation domain of BZLF1. Although a functional relationship between BZLF1 and PKC could be mediated by RACKs, RACK1 did not have a detectable effect on the phosphorylation status of BZLF1 in in vitro or in vivo phosphorylation assays. We suggest that RACK1 may act as a scaffolding protein on BZLF1 independently of activated PKCs.

L15 ANSWER 13 OF 26 MEDLINE on STN
ACCESSION NUMBER: 2000491127 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11043577
TITLE: Androgen receptor nuclear translocation is facilitated by the f-actin cross-linking protein filamin.
AUTHOR: Ozanne D M; Brady M E; Cook S; Gaughan L; Neal D E; Robson C N
CORPORATE SOURCE: Prostate Research Group, School of Surgical and Reproductive Sciences, Medical School, University of Newcastle upon Tyne, England.
SOURCE: Molecular endocrinology (Baltimore, Md.), (2000 Oct) 14 (10) 1618-26.
Journal code: 8801431. ISSN: 0888-8809.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010208

AB The human androgen receptor (hAR) is a ligand-dependent transcription factor responsible for the development of the male phenotype. The mechanism whereby nuclear translocation of the hAR is induced by its natural ligand 5alpha-dihydrotestosterone is a phenomenon not fully understood. The two-hybrid **interaction trap assay** has been used to isolate proteins that interact with the hAR in an attempt to identify molecules involved in hAR transactivation and movement. We have identified the actin-binding protein filamin, a 280-kDa component of the cytoskeleton, as an hAR interacting protein. This interaction is ligand independent but is enhanced in its presence. The functional significance of this interaction was analyzed using a cell line deficient in filamin via transient expression of a green fluorescent protein-hAR chimera. In filamin-deficient cells this revealed that hAR remained cytoplasmic even after prolonged exposure to synthetic ligand. Nuclear shuttling was restored when this cell line regained wild-type expression of filamin. These data suggest a novel role for filamin, implicating it as an important molecule in AR movement from the cytoplasm to the nucleus.

L15 ANSWER 14 OF 26 MEDLINE on STN DUPLICATE 6
ACCESSION NUMBER: 2000183695 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10717484

TITLE: Identification of drosophila bicoid-interacting proteins using a custom **two-hybrid selection.**
AUTHOR: Zhu W; Hanes S D
CORPORATE SOURCE: Department of Biomedical Sciences, School of Public Health, State University of New York at Albany, Albany, NY, USA.
SOURCE: Gene, (2000 Mar 21) 245 (2) 329-39.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF096866; GENBANK-AF097636
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000512
Last Updated on STN: 20021227
Entered Medline: 20000502

AB Bicoid directs pattern formation in the developing Drosophila embryo, and does so by performing two seemingly unrelated tasks; it activates transcription and represses translation. To understand how Bicoid carries out this dual role, we sought to identify Bicoid-ancillary proteins that might mediate Bicoid's function in transcription or translation. We used a customized version of the two-hybrid method and found two Bicoid-interacting proteins, Bin1 and Bin3, both of which interact with Bicoid in vitro. Bin1 is similar to a human protein (SAP18) involved in transcription regulation, and Bin3, described in this paper, is similar to a family of protein methyltransferases that modify RNA-binding proteins. Given that Bicoid's role as a translation regulator requires RNA binding, we suggest that the Bicoid-interacting methyltransferase might be important for that role. The custom two-hybrid method we used, in which Bicoid is bound to DNA via its own DNA binding domain, rather than via a **fusion-protein** tether, should be **generally** applicable to other DNA binding proteins.

L15 ANSWER 15 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 1999-327402 [27] WPIDS
DOC. NO. NON-CPI: N1999-245541
DOC. NO. CPI: C1999-096984
TITLE: cDNA encoding CIITA-interacting protein 104.
DERWENT CLASS: B04 D16 P14 S03
INVENTOR(S): GLIMCHER, L H; ZHOU, H
PATENT ASSIGNEE(S): (HARD) HARVARD COLLEGE; (GLIM-I) GLIMCHER L H; (ZHOU-I) ZHOU H
COUNTRY COUNT: 84
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9924570	A1	19990520	(199927)*	EN	77
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZW					
AU 9912861	A	19990531	(199941)		
EP 961828	A1	19991208	(200002)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
JP 2001508313	W	20010626	(200140)		92
AU 736150	B	20010726	(200149)		

US 2002019514 A1 20020214 (200214)
US 6410261 B1 20020625 (200246)
US 2002146806 A1 20021010 (200269)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9924570	A1	WO 1998-US22934	19981028
AU 9912861	A	AU 1999-12861	19981028
EP 961828	A1	EP 1998-956308	19981028
		WO 1998-US22934	19981028
JP 2001508313	W	WO 1998-US22934	19981028
		JP 1999-526487	19981028
AU 736150	B	AU 1999-12861	19981028
US 2002019514	A1	US 1997-965272	19971106
US 6410261	B1	US 1997-965272	19971106
US 2002146806	A1 Cont of	US 1997-965272	19971106
		US 2002-121882	20020412

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9912861	A Based on	WO 9924570
EP 961828	A1 Based on	WO 9924570
JP 2001508313	W Based on	WO 9924570
AU 736150	B Previous Publ.	AU 9912861
	Based on	WO 9924570
US 2002146806	A1 Cont of	US 6410261

PRIORITY APPLN. INFO: US 1997-965272 19971106; US 2002-121882 20020412

AN 1999-327402 [27] WPIDS

AB WO 9924570 A UPAB: 19990714

NOVELTY - isolated nucleic acid molecule (I) comprising a nucleotide sequence encoding CIITA-interacting protein 104 (CIP104) is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) isolated nucleic acid molecules that:

(a) are at least 15 nucleotides in length which hybridizes under stringent conditions to a nucleic acid molecule comprising the 4236 bp sequence (given in the specification);

(b) comprise the coding region of the 4236 bp sequence; or

(c) encode a 945 amino acid sequence (given in the specification);

(2) a vector comprising (I);

(3) a host cell containing the vector of (b);

(4) production of CIP104 by culturing the host cell above, in a suitable medium until CIP104 is produced;

(5) an isolated CIP104 protein;

(6) a **fusion protein** comprising a CIP104 polypeptide operatively linked to a non-CIP104 polypeptide;

(7) antibodies that specifically bind CIP104; a non-human transgenic animal that contains cells carrying a **transgene** encoding CIP104; detecting the presence of CIP104 activity in a biological sample;

(8) modulating CIP104 activity in a cell; and

(9) identifying a compound that modulates the activity of CIP104.

ACTIVITY - Immunomodulatory.

MECHANISM OF ACTION - Transcription Enhancer.

USE - CIP104 activity can be detected by use of a labeled nucleic acid probe capable of hybridizing to CIP104 mRNA or using a labeled

antibody specific for the CIP104 protein (claimed). CIP104 activity can be modulated using CIP104 antibodies or antisense nucleotide sequences to the CIP104 mRNA coding strand (claimed). Modulation of CIP104 activity may be beneficial in clinical situations requiring modulation of MHC class II **gene** expression, e.g. an immunodeficiency, infectious disease, cancer, autoimmune disease or transplantation.

DESCRIPTION OF DRAWING(S) - The effect of increasing amounts of CIP104 on transactivation of human MHC class II DR alpha promoter, in the absence or presence of CIITA.

Dwg.3/4

L15 ANSWER 16 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 1999-153316 [13] WPIDS
DOC. NO. CPI: C1999-045203
TITLE: Isolating nucleic acids encoding proteins comprising a signal peptide - by translating RNA and isolating translated RNA that is associated with microsomes, useful as therapeutic agents.
DERWENT CLASS: B04 D16
INVENTOR(S): KINOSHITA, N; KIRSCHNER, M W
PATENT ASSIGNEE(S): (HARD) HARVARD COLLEGE
COUNTRY COUNT: 20
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9905256	A2	19990204	(199913)*	EN	45
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA					
US 6066460	A	20000523	(200032)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9905256	A2	WO 1998-US15394	19980724
US 6066460	A Provisional	US 1997-53586P	19970724
		US 1998-121920	19980724

PRIORITY APPLN. INFO: US 1997-53586P 19970724; US 1998-121920 19980724
AN 1999-153316 [13] WPIDS
AB WO 9905256 A UPAB: 19990331
Isolation of nucleic acid (I) that encodes a protein (II) having a signal peptide (SP) comprises isolating RNA molecules (III) that are associated with microsomes under conditions where (III) is at least partly translated. Also claimed are: (1) a library of (I) encoding (II) comprising SP; (2) (I) isolated by the above method; and (3) (II) encoded by (I).

USE - (I) and (II) are useful therapeutically, typically (II) are cell growth factors such as cytokines, interleukins, colony-forming factors, possibly useful in treatment of cancer. (I) are also used: as tissue and molecular weight markers; as chromosome tags; to detect possible **genetic** disorders; as hybridisation probes to identify related nucleic acid; as primers for DNA fingerprinting; to **generate** antibodies; and in **interaction trap assays** to identify **gene** encoding specific binding agents. (II) are useful in drug screening, for raising antibodies (e.g. for use as immunoassay reagents) and to induce an immune response.

ADVANTAGE - The method is more efficient and reliable than the sequence trap system. It does not involve formation of a **fusion protein** (rather natural **proteins** are **selected**) and (II) do not have to be secreted.
Dwg.0/4

L15 ANSWER 17 OF 26 MEDLINE on STN
ACCESSION NUMBER: 2000059178 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10593605
TITLE: Cloning of a Schizosaccharomyces pombe homologue of elongation factor 1 alpha by **two-hybrid selection** of calmodulin-binding **proteins.**
AUTHOR: Rasmussen C; Wiebe C
CORPORATE SOURCE: Department of Anatomy and Cell Biology, University of Saskatchewan, Saskatoon, Canada.. colin@pombe.usask.ca
SOURCE: Biochemistry and cell biology = Biochimie et biologie cellulaire, (1999) 77 (5) 421-30.
Journal code: 8606068. ISSN: 0829-8211.
PUB. COUNTRY: Canada
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U42189
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000124
Last Updated on STN: 20000124
Entered Medline: 20000107

AB This study reports the cloning and characterization of a cDNA encoding elongation factor 1-alpha (EF1alpha) from the yeast Schizosaccharomyces pombe. The cDNA was cloned from an Schizosaccharomyces pombe expression library by a **two-hybrid selection** for clones encoding calmodulin (CaM)-binding proteins. The predicted protein is highly homologous to mammalian EF1alpha, indicating a strong tendency towards conservation of the primary amino acid sequence. The protein was expressed as a glutathione S-transferase fusion in both bacteria and in Schizosaccharomyces pombe. The bacterial protein was shown by solution assay to compete with CaM kinase II for CaM. The CaM binding domain was localized to the C-terminus of the protein by this method. Expression of full-length EF1alpha in vivo caused an increase in cell cycle length and a decreased rate of growth as evidenced by a lack of elongated cells in slowly dividing cultures. This effect appears to involve CaM binding because a truncation mutant version of EF1alpha lacking the CaM binding domain did not cause cell cycle delay.

L15 ANSWER 18 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 1998-414109 [35] WPIDS
DOC. NO. CPI: C1998-125060
TITLE: New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto immune disease.
DERWENT CLASS: B04 D16
INVENTOR(S): COLLINS, M; DONALDSON, D D; NEBEN, T; WHITTERS, M
PATENT ASSIGNEE(S): (GEMY) GENETICS INST INC
COUNTRY COUNT: 82
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9831811	A1	19980723	(199835)*	EN	37

RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA
PT SD SE SZ UG ZW
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE
GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG
MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG
US UZ VN YU ZW

AU 9857338	A	19980807 (199901)	
EP 1005552	A1	20000607 (200032)	EN
R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE			
JP 2001508309	W	20010626 (200140)	44

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9831811	A1	WO 1998-US334	19980115
AU 9857338	A	AU 1998-57338	19980115
EP 1005552	A1	EP 1998-901207	19980115
		WO 1998-US334	19980115
JP 2001508309	W	JP 1998-534435	19980115
		WO 1998-US334	19980115

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9857338	A	Based on	WO 9831811
EP 1005552	A1	Based on	WO 9831811
JP 2001508309	W	Based on	WO 9831811

PRIORITY APPLN. INFO: US 1997-784863 19970116

AN 1998-414109 [35] WPIDS

AB WO 9831811 A UPAB: 19981001

Isolated nucleic acid (I) is: (a) nucleotides (nt) 242-1396 of a 1656 bp sequence (S1); (b) nt 71-1225 of a 1579 bp sequence (S2) (sequences are given in the specification); (c) a sequence equivalent to (a) or (b) within the **degeneracy** of the **genetic** code; (d) a sequence that hybridises under stringent conditions to, or is a species homologue of, (a) or (b), or (e) an allelic variant of (a) or (b). Also new are: (A) host cells, particularly mammalian, transformed with (I); (B) isolated U4 proteins (II) of: (i) 425 amino acids (aa) or its 41-425 aa fragment, or (ii) 408 aa, or its 24-408 aa fragment, or their fragments with the activity of a U4 haematopoietin receptor superfamily chain (sequences are given in the specification); (C) antibodies (Ab) specific for (II); (D) any nucleic acid encoding (II), and (E) **fusion proteins** (FP) that include (II).

USE - Cells of (A) are used to produce recombinant U4 protein. (II) are used: (i) to screen for specific binding agents; (ii) to raise Ab; (iii) as reagents for assays and as tissue markers; (iv) for isolation of cognate ligands and receptors, and (v) in pharmaceutical compositions which may modify cell proliferation or differentiation; stimulate or suppress the immune system (e.g. for treating immune deficiency, inherited or the result of infection; autoimmune diseases, cancer, allergy); in cases of organ transplants; to regulate haematopoiesis (e.g. for treating myeloid or lymphoid cell deficiency in cases of (aplastic) anaemia, thrombocytopaenia, or in conjunction with radiation or chemotherapy). (I) are useful as tissue, molecular weight or chromosomal markers; as primers for **genetic** fingerprinting; to **generate** anti-protein antibodies, in **interaction trap assays**. (I) and (II) can also be used as nutritional sources or supplements, and Ab

are used as assay reagents or, where neutralising, for treatment of the specified diseases. (II) are administered by injection or inhalation, particularly intravenously at 0.1 mu g to 0.1 mg/kg.
Dwg.0/0

L15 ANSWER 19 OF 26 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 1998-179061 [16] WPIDS
DOC. NO. CPI: C1998-057500
TITLE: Polypeptide **interaction trap assay** - using prokaryotic host cells producing **fusion proteins** which activate reporter **genes.**
DERWENT CLASS: B04 D16
INVENTOR(S): DOVE, S; HOCHSCHILD, A; JOUNG, J K; JOUNG, K J
PATENT ASSIGNEE(S): (HARD) HARVARD COLLEGE
COUNTRY COUNT: 76
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9807845	A1	19980226	(199816)*	EN	63
RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN					
AU 9741596	A	19980306	(199830)		
US 5925523	A	19990720	(199935)		
US 6200759	B1	20010313	(200120)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9807845	A1		WO 1997-US14860	19970822
AU 9741596	A		AU 1997-41596	19970822
US 5925523	A	Provisional	US 1996-24484P	19960823
		CIP of	US 1997-918612	19970822
			US 1997-920015	19970826
US 6200759	B1	Provisional	US 1996-24484P	19960823
		CIP of	US 1997-918612	19970822
		Cont of	US 1997-920015	19970826
			US 1999-296204	19990421

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9741596	A	Based on	WO 9807845
US 6200759	B1	Cont of	US 5925523

PRIORITY APPLN. INFO: US 1996-24484P 19960823; US 1997-918612 19970822; US 1997-920015 19970826; US 1999-296204 19990421
AN 1998-179061 [16] WPIDS
AB WO 9807845 A UPAB: 19980421
Detecting interaction between a first test polypeptide and second test polypeptide comprises:
(a) providing an interaction trap system (ITS) including a

prokaryotic host cell which contains:

(i) a reporter **gene** operably linked to a transcriptional regulatory sequence which includes a binding site (DBD recognition element) for a DNA-binding domain;

(ii) a first chimeric **gene** which encodes a first **fusion protein** (FP), the first FP including a DNA-binding domain and first test polypeptide; (iii) a second chimeric **gene** which encodes a second FP including an activation tag which activates transcription of a reporter **gene** when localised to the vicinity of the DBD recognition element, where interaction of the first FP and second FP in the host cell results in measurably greater expression of the reporter **gene**;

(b) measuring expression of the reporter **gene**, and

(c) comparing the level of expression of the reporter **gene** to a level of expression in a control ITS in which one or both of the first and second test polypeptides are missing from the first and second FPs and resulting FPs do not interact; where a statistically significant increase in the level of expression is indicative of an interaction between the first and second test polypeptide portions of the FPs.

Also claimed are:

(1) a kit for the above which comprises:

(a) a first vector for encoding a first FP (bait FP) which comprises a first **gene** which comprises:

(i) transcriptional and translational elements which direct expression in a prokaryotic host cell;

(ii) a DNA sequence that encodes a DNA-binding domain and which is functionally associated with the transcriptional and translational elements of the first **gene**, and

(iii) a device for inserting a DNA sequence encoding a first test polypeptide into the first vector in such a manner that the first test polypeptide is capable of being expressed in-frame as part of a bait FP containing the DNA binding domain;

(b) a second vector for encoding a second FP (prey FP) which comprises a second **gene** which comprises:

(i) transcriptional and translational elements which direct expression in a prokaryotic host cell;

(ii) a DNA sequence that encodes a polymerase interaction domain (PID) which forms active RNA polymerase complexes in the prokaryotic host cell, the PID DNA sequence being functionally associated with the transcriptional and translational elements of the second **gene**, and

(iii) a device for inserting a DNA sequence encoding a second test polypeptide into the second vector in such a manner that the second test polypeptide is capable of being expressed in-frame as part of a prey FP containing the PID, and

(c) a prokaryotic host cell containing a reporter **gene** having a binding site (DBD recognition element) for a DNA-binding domain, where the reporter **gene** expresses a detectable protein when a prey FP interacts with a bait FP bound to the DBD recognition element, the host cell being incapable of expressing any appreciable level of a protein having the function of, (i) the first marker **gene**, (ii) the second marker **gene**, (iii) the DNA-binding domain, and (iv) the PID, where binding of the first test polypeptide and the second test polypeptide in the host cell results in measurably greater expression of the reporter **gene** that the simultaneous presence of the DNA-binding domain and the PID in the absence of an interaction between the first test polypeptide and the second test polypeptide, and

(2) a method of isolating a nucleic acid encoding a polypeptide with a **selected protein** target, which comprises:

(a) providing an ITS including a variegated population of prokaryotic

host cells which each include:

(i) a reporter **gene** operably linked to a transcriptional regulatory sequence which includes a binding site (DBD recognition element) for a DNA-binding domain;

(ii) a first chimeric **gene** which encodes a first FP, the first FP including a DNA-binding domain and first test polypeptide;

(iii) a second chimeric **gene** which encodes a second FP including an activation tag activates transcription of the reporter **gene** when localised to the vicinity of the DBD recognition element, where interaction of the first FP and second FP in the host cell results in measurably greater expression of the reporter **gene**, and one of the first or second chimeric **genes** is present in the host cell population as a variegated population with respect to sequence encoding test polypeptides;

(b) measuring expression of the reporter **gene** under conditions where a statistically significant increase in the level of expression of the reporter **gene** is indicative of an interaction between the first and second test polypeptide portions of the FPs, and

(c) selecting cells from the host cell population on the basis of the level of expression of the reporter **gene**.

USE - The method is used for detecting interactions between two polypeptides, e.g. for **generating** protein linkage maps, for identifying protein-protein targets, and for **general** cloning strategies.

ADVANTAGE - The use of prokaryotic host cells, which are easily propagated to **generate** an ITS provides a system which is easy to manipulate. The short doubling times for bacteria will often provide for development of a signal in the ITS in a shorter time period than would be obtained with a eukaryotic ITS.

Dwg.0/6

L15 ANSWER 20 OF 26 MEDLINE on STN

ACCESSION NUMBER:	1999006925 MEDLINE
DOCUMENT NUMBER:	PubMed ID: 9792439
TITLE:	Inhibition of the apolipoprotein B mRNA editing enzyme-complex by hnRNP C1 protein and 40S hnRNP complexes.
AUTHOR:	Greeve J; Lellek H; Rautenberg P; Greten H
CORPORATE SOURCE:	Medizinische Klinik, Universitats-Krankenhaus Eppendorf, Hamburg, Germany.
SOURCE:	Biological chemistry, (1998 Aug-Sep) 379 (8-9) 1063-73. Journal code: 9700112. ISSN: 1431-6730.
PUB. COUNTRY:	GERMANY: Germany, Federal Republic of
DOCUMENT TYPE:	Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:	English
FILE SEGMENT:	Priority Journals
ENTRY MONTH:	199812
ENTRY DATE:	Entered STN: 19990115 Last Updated on STN: 20021218 Entered Medline: 19981223

AB The apolipoprotein (apo) B mRNA can be modified by a posttranscriptional base change from cytidine to uridine at nucleotide position 6666. This editing of apo B mRNA is mediated by a specific enzyme-complex of which only the catalytic subunit APOBEC-1 (apo B mRNA editing enzyme component 1) has been cloned and extensively characterized. In this study, **two-hybrid selection** in yeast identified hnRNP C1 protein to interact with APOBEC-1. Recombinant hnRNP C1 protein inhibited partially purified apo B mRNA editing activity from rat small intestine and bound specifically to apo B sense RNA around the editing site. The inhibition of apo B mRNA editing by hnRNP C1 protein was not due to masking of the RNA substrate as the mutant protein M104 spanning

the RNA-binding domain of hnRNP C1 protein bound strongly to the apo B RNA, but did not inhibit the editing reaction. The apo B mRNA editing enzyme-complex of rat liver nuclear extracts sedimented in sucrose density gradients around 22-27S, but did not contain hnRNP C1 protein that was found exclusively within 40S hnRNP complexes. The removal of 40S hnRNP complexes increased the activity of the 22-27S editing enzyme-complex. Adding back 40S hnRNP complexes with hnRNP C1 protein resulted in an inhibition of the 22-27S apo B mRNA editing enzyme-complex, while addition of 18S fractions had no effect. In conclusion, hnRNP C1 protein identified by **two-hybrid selection** in yeast is a potent inhibitor of the apo B mRNA editing enzyme-complex. The abundant hnRNP C1 protein, which is contiguously deposited on nascent pre-mRNA during transcription and is involved in spliceosome assembly and mRNA splicing, is a likely regulator of the editing of apo B mRNA which restricts the activity of APOBEC-1 to limited and specific editing events.

L15 ANSWER 21 OF 26 MEDLINE on STN
ACCESSION NUMBER: 1998300000 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9636371
TITLE: HHR23A, the human homologue of the yeast repair protein RAD23, interacts specifically with Vpr protein and prevents cell cycle arrest but not the transcriptional effects of Vpr.
AUTHOR: Gragerov A; Kino T; Ilyina-Gragerova G; Chrousos G P; Pavlakis G N
CORPORATE SOURCE: ABL-Basic Research Program, NCI-Frederick Cancer Research and Development Center, Maryland 21702-1201, USA.
SOURCE: Virology, (1998 Jun 5) 245 (2) 323-30.
Journal code: 0110674. ISSN: 0042-6822.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; AIDS
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980723
Last Updated on STN: 19980723
Entered Medline: 19980714

AB Yeast **two-hybrid selection** of **proteins** interacting with human immunodeficiency virus type 1 Vpr identified HHR23A, a human homologue of the yeast DNA repair protein RAD23, as a specific interactor. A small 57-amino-acid C-terminal portion of HHR23A was sufficient for Vpr interaction. When introduced into human cells by transfection, full-length HHR23A or its C-terminal fragments were able to alleviate Vpr-induced cell cycle arrest, suggesting that HHR23A may participate in the pathway leading to G2 arrest by Vpr. We have also examined the effects of HHR23 on the recently identified **transcription coactivator** function of Vpr. The two Vpr functions are independent, since we have identified mutants lacking either the cell cycle arrest or the coactivator function. Our analysis showed that excess of HHR23A does not affect the coactivator function of Vpr, while it affects the cell cycle arresting function. Therefore, a simple sequestering model for Vpr in the presence of excess HHR23A is not supported. We propose that the interaction of HHR23A with Vpr may affect specifically pathways leading to cell cycle regulation.

L15 ANSWER 22 OF 26 MEDLINE on STN DUPLICATE 7
ACCESSION NUMBER: 97413835 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9268371
TITLE: Specific interactions of the autoantigen L7 with multi-zinc finger protein ZNF7 and ribosomal protein S7.

AUTHOR: Witte S; Krawinkel U
CORPORATE SOURCE: Fakultat fur Biologie, Universitat Konstanz, Postfach 5560, 78434 Konstanz, Germany.. stephan.witte@uni-konstanz.de
SOURCE: Journal of biological chemistry, (1997 Aug 29) 272 (35) 22243-7.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199710
ENTRY DATE: Entered STN: 19971013
Last Updated on STN: 19971013
Entered Medline: 19971002

AB The eucaryotic protein L7, which associates with the large subunit of ribosomes, has been shown to be a major autoantigen in systemic autoimmune arthritis. The N terminus carries a sequence motif that is similar to the leucine zipper domain of eucaryotic transcription factors. This domain promotes the **homodimerization** of protein L7 through alpha-helical coiled-coil formation and binds to distinct mRNAs, thereby inhibiting their cell-free translation. Using a yeast **two-hybrid selection**, we have identified from a Jurkat T lymphoma cDNA library ribosomal protein S7 and the multi-zinc finger protein ZNF7 as proteins that interact with protein L7. A fragment of L7 carrying the leucine zipper-like domain is fully sufficient to mediate these interactions. Their potential biological significance is indicated by low apparent dissociation constants of S7-L7 (15 x 10(-9) M) and, respectively, ZNF7-L7 (2 x 10(-9) M) complexes and co-immunoprecipitation of proteins S7, ZNF7, and L7 from a cell lysate with an anti-L7 antibody. We also show that ZNF7-like L7 and S7 can exist in a ribosome-bound form. This study provides further evidence suggesting that L7 is involved in translational regulation through interactions with components of the translational apparatus.

L15 ANSWER 23 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1998:47923 BIOSIS
DOCUMENT NUMBER: PREV199800047923
TITLE: Specific interactions between the K domains of AG and AGLs, members of the MADS domain family of DNA binding proteins.
AUTHOR(S): Fan, Hua-Ying; Hu, Yi; Tudor, Matthew; Ma, Hong [Reprint author]
CORPORATE SOURCE: Cold Spring Harbor Lab., 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
SOURCE: Plant Journal, (Nov., 1997) Vol. 12, No. 5, pp. 999-1010. print.
ISSN: 0960-7412.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 27 Jan 1998
Last Updated on STN: 27 Jan 1998

AB MADS domain (for MCM1, AG, DEFA and SRF) proteins are regulatory proteins found in all major eukaryotic kingdoms. Plant MADS domain regulatory proteins have a region of moderate sequence similarity that has been designated as the K domain, and its predicted coiled-coil structure suggests a role in establishing a protein-protein interaction. In vivo studies with the Arabidopsis AGAMOUS (AG) protein have indicated that the K domain is important for AG function. Using a bait **fusion protein** containing the K domain and the C-terminal region of AG in a yeast **two-hybrid selection**, 156 clones that encode potential AG-interacting proteins were identified. These

clones each encode one of four highly related MADS domain proteins: AGL2, AGL4, AGL6 and AGL9. Additional analysis showed that the K domain of AG alone was able to bind the K domains of these AGLs. This binding was further confirmed by immunoprecipitation experiments using in vitro synthesized AG and AGL K domains. These results strongly suggest that AG interacts with AGL2, AGL4, AGL6 and AGL9 in vivo. Based on these results and previous observations, it is proposed that the AG function requires interaction with at least one of these AGL proteins, and such interactions contribute to the functional specificity of the AG protein.

L15 ANSWER 24 OF 26 MEDLINE on STN DUPLICATE 8
ACCESSION NUMBER: 97113044 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8943297
TITLE: **Transcription activation** by the bacteriophage Mu Mor protein requires the C-terminal regions of both alpha and sigma70 subunits of Escherichia coli RNA polymerase.
AUTHOR: Artsimovitch I; Murakami K; Ishihama A; Howe M M
CORPORATE SOURCE: Department of Microbiology and Immunology, University of Tennessee-Memphis, Memphis, Tennessee 38163, USA.. mhowe@utmem1.utmem.edu
SOURCE: Journal of biological chemistry, (1996 Dec 13) 271 (50) 32343-8.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19980206
Entered Medline: 19970117

AB Middle transcription of bacteriophage Mu requires Escherichia coli RNA polymerase and a Mu-encoded protein, Mor. Consistent with these requirements, the middle promoter, Pm, has a -10 hexamer but lacks a recognizable -35 hexamer. Interactions between Mor and RNA polymerase were studied using in vitro transcription, DNase I footprinting, and the yeast interaction trap system. We observed reduced promoter activity in vitro using reconstituted RNA polymerases with C-terminal deletions in alpha or sigma70. As predicted if alpha were binding to Pm, we detected a polymerase-dependent footprint in the -60 region. Reconstituted RNA polymerases containing Ala substitutions in the alpha C-terminal domain were used to assay Mor-dependent transcription from Pm in vitro. The D258A substitution and alpha deletion gave large reductions in activation, whereas the L262A, R265A, and N268A substitutions caused smaller reductions. The **interaction trap assay** revealed weak interactions between Mor and both alpha and sigma70; consistent with a key role of alpha-D258, the D258A substitution abolished interaction, whereas the R265A substitution did not. We propose that: (i) alpha-D258 is a Mor "contact site"; and (ii) residues Leu-262, Arg-265, and Asn-268 indirectly affect Mor-polymerase interaction by stabilizing the ternary complex via alpha-DNA contact.

L15 ANSWER 25 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1996:53343 BIOSIS
DOCUMENT NUMBER: PREV199698625478
TITLE: Cloning of a Schizosaccharomyces pombe cDNA for elongation factor 1-alpha by **two hybrid selection** of calmodulin binding **proteins.**
AUTHOR(S): Wiebe, C. A. [Reprint author]; Rasmussen, C.

CORPORATE SOURCE: Dep. Biochem., Univ. Alberta, Edmonton, AB T6G 2H7, Canada
SOURCE: Molecular Biology of the Cell, (1995) Vol. 6, No. SUPPL., pp. 257A.
Meeting Info.: Thirty-fifth Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 9-13, 1995.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 2 Feb 1996
Last Updated on STN: 3 Feb 1996

L15 ANSWER 26 OF 26 MEDLINE on STN DUPLICATE 9
ACCESSION NUMBER: 95032035 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7945309
TITLE: Nuclear localization of p185neu tyrosine kinase and its association with **transcriptional transactivation.**
AUTHOR: Xie Y; Hung M C
CORPORATE SOURCE: Department of Tumor Biology, University of Texas M. D. Anderson Cancer Center, Houston 77030.
CONTRACT NUMBER: CA58880 (NCI)
CA60856 (NCI)
SOURCE: Biochemical and biophysical research communications, (1994 Sep 30) 203 (3) 1589-98.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199410
ENTRY DATE: Entered STN: 19941222
Last Updated on STN: 20000303
Entered Medline: 19941031

AB The rat neu **protooncogene** encodes a 185 kD transmembrane protein (p185neu), which is a member of the epidermal growth factor receptor (EGFr) family. In searching for the signaling transducer of p185neu by using a **two-hybrid selection** system, we found, surprisingly, that the cytoplasmic domain of p185neu, when fused to the DNA-binding domain of GAL4 (amino acids 1-147), functioned as a **transcriptional activator.** We subsequently observed nuclear localization of p185neu. Interestingly, nuclear p185neu has a much higher extent of tyrosine phosphorylation than its nonnuclear counterpart. Our results suggest that a transmembrane receptor tyrosine kinase may enter the nucleus and be involved in **transcriptional activation.** This novel finding unveils a clue in the understanding of the mechanism of receptor tyrosine kinase-mediated signal transduction.

=> d ibib abs ind l4 1-2

L4 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:658658 HCAPLUS
DOCUMENT NUMBER: 137:197850
TITLE: Methods and compositions for interaction trap assays
INVENTOR(S): **Joung, J. Keith; Miller, Jeffrey; Pabo, Carl O.**
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 61 pp., Cont.-in-part of U.S. Ser. No. 858,852.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002119498	A1	20020829	US 2001-990762	20011114
US 2003044787	A1	20030306	US 2001-858852	20010516

PRIORITY APPLN. INFO.: US 2000-204509P P 20000516
US 2001-858852 A2 20010516

AB The invention concerns methods and compns. for interaction trap assays for detecting protein-protein, protein-DNA, or protein-RNA interactions. The methods and compns. of the invention may also be used to identify agents which may agonize or antagonize a protein-protein, protein-DNA, or protein-RNA interaction. In certain embodiments, the interaction trap system of the invention is useful for screening libraries with greater than 107 members. In other embodiments, the interaction trap system of the invention is used in conjunction with flow cytometry. The invention further provides a means for simultaneously screening a target protein or nucleic acid sequence for the ability to interact with two or more test proteins or nucleic acids.

IC ICM G01N033-53
ICS G01N033-567; C12Q001-68
NCL 435007200
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 3
ST protein DNA RNA interaction flow cytometry peptide library; fusion protein genetic methods reporter gene transcription
IT Genetic element
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(DBD (DNA binding domain) recognition element; methods and compns. for interaction trap assays)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(DNA-binding; methods and compns. for interaction trap assays)
IT Cytometry
(FACS (fluorescence-activated cell sorting); methods and compns. for interaction trap assays)
IT Proteins
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(complexes, with DNA; methods and compns. for interaction trap assays)
IT Proteins
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(complexes, with RNA; methods and compns. for interaction trap assays)
IT Proteins

RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(complexes, with proteins; methods and compns. for interaction trap assays)

IT Reporter gene
RL: PRP (Properties)
(expression of; methods and compns. for interaction trap assays)

IT Cell proliferation
Dimerization
Genetic methods
Molecular recognition
Peptide library
Prokaryote
Transcription, genetic
(methods and compns. for interaction trap assays)

IT Fusion proteins (chimeric proteins)
Polynucleotides
Transcription factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(methods and compns. for interaction trap assays)

IT Chimeric gene
RL: PRP (Properties)
(methods and compns. for interaction trap assays)

IT Protein motifs
(zinc finger, Cys2His2; methods and compns. for interaction trap assays)

IT 452379-03-2 452379-04-3
RL: PRP (Properties)
(unclaimed nucleotide sequence; methods and compns. for interaction trap assays)

IT 452379-05-4 452379-06-5 452379-07-6 452379-08-7 452379-09-8
452379-13-4 452379-14-5 452379-15-6
RL: PRP (Properties)
(unclaimed sequence; methods and compns. for interaction trap assays)

L4 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:851433 HCAPLUS
DOCUMENT NUMBER: 136:1569
TITLE: Interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions
INVENTOR(S): **Joung, J. Keith; Miller, Jeffrey; Pabo, Carl O.**
PATENT ASSIGNEE(S): Massachusetts Institute of Technology, USA
SOURCE: PCT Int. Appl., 196 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001088197	A2	20011122	WO 2001-US15718	20010516
WO 2001088197	A3	20031231		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ,

VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 2000-204509P P 20000516

AB The present invention provides methods and compns. for interaction trap assays for detecting protein-protein, protein-DNA, or protein-RNA interactions using prokaryotic or microbial eukaryotic hosts. The methods and compns. of the invention may also be used to identify agents which may agonize or antagonize a protein-protein, protein-DNA, or protein-RNA interaction. In certain embodiments, the interaction trap system of the invention is useful for screening libraries with greater than 107 members. In other embodiments, the interaction trap system of the invention is used in conjunction with flow cytometry. The invention further provides a means for simultaneously screening a target protein or nucleic acid sequence for the ability to interact with two or more test proteins or nucleic acids. In one form, the screening involves the use of a selectable marker allowing screening of large nos. of cells without the need to scan for a colorimetric marker. In a second form, screening of a colorimetric marker is by flow cytometry. Screening of a library of 108 members in Escherichia coli for C2H2 zinc finger variants is demonstrated.

IC ICM C12Q001-68

CC 3-1 (Biochemical Genetics)

ST two hybrid assay selectable marker screening; zinc finger variant selection screening; prokaryotic host two hybrid screening; FACS screening interaction trap assay

IT Proteins
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(BLIP, as β-lactamase inhibitor in screening for β-lactam resistance; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(CTX1, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Cytometry
(FACS (fluorescence-activated cell sorting), in screening of reporter gene expression; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Transcription factors
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(GAL4, fusion products; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(HIS3, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(NRE (neg. regulatory element), selection of zinc fingers binding; interaction trap assays using selectable markers to screen large

libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(OXA1, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(OXA2, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(OXA3, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PSE1, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PSE2, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PSE3, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PSE4, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(SHV1, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(TATA box, selection of zinc fingers binding; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(TEM1, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(TEM2, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(aadA, as reporter; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Magnetic particles
(affinity ligand-bearing, in purification of marker presenting cells; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Carbohydrates, biological studies
Natural products
Oligonucleotides
Peptides, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(as effectors of protein interactions, screening for; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Antibiotic resistance
(as marker in selectable two hybrid assay; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Escherichia coli
(cloning and selection host; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Bacillus (bacterium genus)
Enterococcus
Escherichia
Lactobacillus
Pseudomonas
Salmonella
Serratia
Shigella
Streptococcus
Streptomyces
(expression host; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Cytometry
(flow, in screening of reporter gene expression; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Proteins
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(fluorescent, as reporter; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Drug screening
(for effectors of protein interactions; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Genetic element

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(gene Egr-1 RNA formation factor-responsive element, in reporter gene promoter region; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Transcription factors
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(gene GAL11, fusion products; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Proteins
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(green fluorescent, as reporter; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Affinity chromatography
(in purification of marker presenting cells; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(lacZ, as reporter; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Transcription factors
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(lactose repressors, in regulated expression of genes in two hybrid assays; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(operator, lacO, in regulated expression of genes in two hybrid assays; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(operator, tetO, in regulated expression of genes in two hybrid assays; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Genetic markers
(selectable, regulated expression in two-hybrid screening; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Transcription factors
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(tetR (tetracycline repressor), in regulated expression of genes in two hybrid assays; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)

(tumor antigen p53-responsive element, selection of zinc fingers binding; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Genetic methods
Genomic library
(two-hybrid screening; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Protein motifs
(zinc finger, screening for variants; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Proteins
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(zinc finger-containing, Zif123, fusion products; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Lactams
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(β-, monocyclic, resistance to, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT Antibiotics
(β-lactam, resistance to, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT 367-93-1, IPTG 1665-56-1, Anhydrotetracycline
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(as inducer of chimeric gene expression; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT 26631-90-3, Brobactam 58001-44-8, Clavulanic acid 68373-14-8, Sulbactam 89786-04-9, Tazobactam
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(as β-lactamase inhibitor in screening for β-lactam resistance; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT 9073-60-3, β-Lactamase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(gene for, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT 9014-24-8D, RNA polymerase, fusion products
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT 61-82-5, 3-Aminotriazole 1406-05-9, Penicillins 11111-12-9D, Cephalosporins, derivs. 83200-96-8D, Carbapenem, derivs.
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(resistance to, as selectable marker; interaction trap assays using selectable markers to screen large libraries for protein-protein and

protein-nucleic acid interactions)

IT 375408-15-4, 1: PN: WO0188197 SEQID: 2 unclaimed DNA 375408-16-5, 1: PN: WO0188197 SEQID: 3 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide sequence; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

IT 166029-70-5 375388-89-9 375388-90-2 375388-91-3 375388-92-4
375388-93-5 375388-98-0 375389-03-0 375389-07-4 375389-09-6
375389-11-0 375389-13-2 375389-17-6 375389-18-7 375389-19-8
375389-20-1 375389-22-3 375389-23-4 375389-24-5 375389-25-6
375389-26-7 375389-27-8 375389-28-9 375389-29-0 375389-30-3
375389-31-4 375389-32-5 375389-33-6 375389-34-7 375389-35-8
375389-36-9 375389-37-0 375389-39-2 375389-40-5 375389-41-6
375389-42-7 375389-43-8 375389-44-9 375389-45-0 375389-46-1
375389-47-2 375389-48-3 375389-49-4 375389-50-7 375389-51-8
375389-52-9 375389-53-0 375389-54-1 375389-56-3 375389-57-4
375389-58-5 375389-59-6 375389-60-9 375389-61-0 375389-62-1
375389-63-2 375389-64-3 375389-65-4 375389-66-5 375389-67-6
375389-68-7 375389-69-8 375389-72-3 375389-73-4 375389-74-5
375389-75-6 375389-76-7 375389-77-8 375389-78-9 375408-17-6
375408-18-7 375408-19-8 375408-20-1
RL: PRP (Properties)
(unclaimed sequence; interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions)

L Number	Hits	Search Text	DB	Time stamp
7	116	one adj hybrid adj (assay or system)	USPAT	2004/05/07 20:20
8	64	(one adj hybrid adj (assay or system)) and fusion adj protein	USPAT	2004/05/07 20:20
9	24	((one adj hybrid adj (assay or system)) and fusion adj protein) and (dimer$ or homodimer$)	USPAT	2004/05/07 20:22
10	24	(((one adj hybrid adj (assay or system)) and fusion adj protein) and (dimer$ or homodimer$)) and (activat$ same bind$)	USPAT	2004/05/07 20:22